

REFERENCE
1 other sequences; artificial sequences.

AUTHORS Lyamichev, V. I., Kaiser, M. W. and Lyamicheva, N.
TITLE Pen endonucleases
JOURNAL

FEATURES
Source
1. .43
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 74.0%; Score 14.8; DB 2; Length 43;
Best Local Similarity 88.9%; Pred. No. 1 3e+05; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TAGGCCACAGGTCCA 20
Db 32 TAGGCCACAGGTCCA 15

RESULT 3

BD137038/c
LOCUS BD137038
DEFINITION Method of determining nucleotide sequence and protein encoded by
transfection into host.

ACCESSION BD137038
VERSION BD137038.1
KEYWORDS

Qy 3 TAGGCCACAGGTCCA 20
Db 32 TAGGCCACAGGTCCA 15

SOURCE
ORGANISM unidentified
unclassified sequences.

REFERENCE
1 (bases 1 to 25)
AUTORS Cioppa,G.D., Lindbo,R.L., Pitzmaurice,W.P., Hanley,K.M., Poagu,G.P.
TITLE Method of determining nucleotide sequence and protein encoded by
transfection into host
JOURNAL Patent: JP 200208957-A/17.

COMMENT OS VIRUS
PN JP 200208957-A/17
PD 26-MAR-2002
PR 15-JAN-1999 JP 2000540219
PR 16-JAN-1998 US 09/008186
PI GUY DELIA CIOPPA, ROBERT L ERWIN, WAYNE P
PITZMAURICE, KATHLEEN M
PI HANLEY,
PI MONTO H KUMAGAI, JOHN A LINDBO, DAVID R MCGEE, HAL S PADGETT, PI
GREGORY F POOGUE
PC C12N15/09,C12N15/00,C12O1/68//A01H1/00,C12N5/10,C12N15/00, PC
C12N15/00
PC C12N5/00
CC Method of determining nucleotide sequence and protein encoded
by
transfection into host.

FEATURES
source
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 25;
Best Local Similarity 84.2%; Pred. No. 2 8e+05; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ATGAGCCACAGGTCCA 20
Db 19 ATGAGCCACAGGTCCA 1

REFERENCE
1 Query Match 71.0%; Score 14.2; DB 2; Length 25;
Best Local Similarity 84.2%; Pred. No. 2 8e+05; Indels 0; Gaps 0;

ACCESSION BD210966
DEFINITION Polyvalent unsaturated fatty acid in plant.
VERSION BD210966.1
KEYWORDS

Qy 2 ATGAGCCACAGGTCCA 20
Db 19 ATGAGCCACAGGTCCA 1

SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 25)
AUTORS Kumagai,M.H. and Sverlow,G.G.
TITLE Pichia pastoris alcohol oxidase z2a1 and z2a2 regulatory regions
JOURNAL Patent: US 5641661-A 13-24-JUN-1997;

COMMENT OS Artificial Sequence
PN JP 2002517255-A/1
PD 18-JUN-2002
PR 10-JUN-1999 JP 2000553604
PR 12-JUN-1998 US 60/089043
PI DEBBIE KNOTON
PC C12N15/09,A01H5/00,C12P7/64,C12N15/00
CC Synthetic Oligonucleotide
FH Key
FT Source
1. .41
/organism='Artificial Sequence'.

FEATURES
source
1. .41
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 69.0%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3 9e+05; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAGCCACAGGTCA 17
Db 34 ATGAGCCACAGGTCA 18

RESULT 6
 AR235363/c
 LOCUS AR235363
 DEFINITION Sequence 3 from patent US 6459018.
 ACCESSION AR235363
 VERSION AR235363.1
 KEYWORDS Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Knutson, D.
 DEFINITION Polyunsaturated fatty acids in plants
 JOURNAL Patent: US 6459018-A 3 01-OCT-2002;
 Monsanto Technology LLC; St. Louis, MO
 FEATURES location/Qualifiers 1. .41
 SOURCE /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match 69.0%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATATGAGCCACCGAGTC 17
Db 34 ATATGAGCCACCGAGTC 18

RESULT 7
 CQ792409
 LOCUS CQ792409
 DEFINITION Sequence 154 from Patent WO2004020542.
 ACCESSION CQ792409
 VERSION CQ792409.1
 KEYWORDS Synthetic construct
 SOURCE /organism="synthetic construct"
 ORGANISM

Query Match 69.0%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AATGAGCCACCGAGTC 17
Db 34 ATATGAGCCACCGAGTC 18

RESULT 8
 CQ792359
 LOCUS CQ792359
 DEFINITION Sequence 104 from Patent: WO2004020642.
 ACCESSION CQ792359
 VERSION CQ792359.1
 KEYWORDS Synthetic construct
 SOURCE /organism="synthetic construct"
 ORGANISM

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATATGAGCCACCGAGTC 20
Db 1 AAAGAGCTCCAGTGTCCA 20

RESULT 9
 CS142185/c
 LOCUS CS142185
 DEFINITION Sequence 146 from Patent WO2005071080.
 ACCESSION CS142185
 VERSION CS142185.1
 KEYWORDS Synthetic construct
 SOURCE /organism="synthetic construct"
 ORGANISM

Query Match 68.0%; Score 13.6; DB 2; Length 34;
Best Local Similarity 80.0%; Pred. No. 5e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 AATGAGCCACCGAGTC 20
Db 1 ATTCAGCTCCCAATGTCCA 20

RESULT 10
 AR279075/c
 LOCUS AR279075
 DEFINITION Sequence 208 from patent US 6514694.
 ACCESSION AR279075
 VERSION AR279075.1
 KEYWORDS Unknown.
 SOURCE /organism="unassigned DNA"
 ORGANISM

Query Match 66.0%; Score 13.2; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 8.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TTAGGCCACAGTGTCMA 20
Db 19 TTAACCAACAGTGCCMA 2

RESULT 11
 1
 REFERENCE 1
 AUTHORS McCourt, P., Ghassemian, M., Cutler, S. and Bonetta, D.
 TITLE Stress tolerance and delayed senescence in plants
 JOURNAL Patent: WO 2004020641-A 104 11-MAR-2004;
 Performance Plants, Inc. (CA)
 FEATURES location/Qualifiers 1. .34
 SOURCE /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /ab_xref="taxon:32630"
 /notes="Description of Artificial Sequence: PCR Primer"
 ORIGIN

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATATGAGCCACCGAGTC 20
Db 1 AAAGAGCTCCAGTGTCCA 20

RESULT 12
 1
 REFERENCE 1
 AUTHORS Milhausen, M.J.
 TITLE Methods for the detection of encysted parasites
 JOURNAL Patent: US 6514694-A 208 04-FEB-2003;
 Heska Corporation, Port Collins, CO
 FEATURES location/Qualifiers 1. .22
 SOURCE /organism="unassigned DNA"
 /mol_type="genomic DNA"
 /notes="Description of Artificial Sequence: PCR Primer"
 ORIGIN

ORIGIN	
Query Match	56.0%; Score 13.2; DB 2; Length 22;
Best Local Similarity	83.3%; Pred. No. 8.4e+05; Mismatches 3; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3 TTAGGCCACCAAGTGTCAA 20
Db	1 TGTCGCCAGCAGTGACCAA 18
RESULT 11	A1082793
LOCUS	AY082793
DEFINITION	Homo sapiens clone 101.18 T cell receptor beta chain gene, partial cDNA.
ACCESSION	AY082793
VERSION	AY082793.1
KEYWORDS	GI:29647040
SOURCE	Hom sapiens (human)
ORGANISM	Mammalia; Butharia; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	(bases 1 to 27)
AUTHORS	Lin,W.L., Fincke,J.B., Sharer,L.R., Platoucas,C.D. and Olesek,E.L.
TITLE	Oligoclonal T cells are infiltrating the brain of children with AIDS: sequence analysis revealed high proportions of identical beta-chain T-cell receptor (TCR) transcripts (unpublished)
JOURNAL	2 (bases 1 to 27)
REFERENCE	Lin,W.L., Fincke,J.B., Sharer,L.R., Platoucas,C.D. and Olesek,E.L.
AUTHORS	Direct Submission
TITLE	Submitted (08-JUL-1991) J.L. Casanova, Ludwig Inst. for Cancer Research, Lausanne Branch, Epalinges 1066, SWITZERLAND
JOURNAL	19140, USA
FEATURES	Location/Qualifiers
Source	<p>1. .-27 /organism="Homo sapiens" /mol_type="genomic DNA" /clones="101.18" /note="normal donor PBMC"</p> <p><1. .->27 /product="T cell receptor beta chain" /note="TCR beta; CDR3 region; contains Vbeta 22.1 Dbeta2.1 Jbeta2.5" /codon_start=1 /product="T cell receptor beta chain" /protein_id="PAM03440.1" /db_xref="GI:29647040" /translations="CASSDQETQ"</p>
ORIGIN	
Query Match	66.0%; Score 13.2; DB 5; Length 27;
Best Local Similarity	83.3%; Pred. No. 8.1e+05; Mismatches 3; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3 TTAGGCCACCAAGTGTCAA 20
Db	1 TGTCGCCAGCAGTGACCAA 18
RESULT 12	X60865.1
MMPSRNA	MMPSRNA
LOCUS	36 bp mRNA linear ROD 07-FEB-1992
DEFINITION	M.musculus rearranged mRNA for T cell receptor beta chain Vbeta13/beta2.7 join.
ACCESSION	X60865
VERSION	X60865.1
KEYWORDS	GI:53624
SOURCE	
ORGANISM	Mammalia; Butharia; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	(bases 1 to 39)
AUTHORS	Nasralla,H.E., Durinovic-Bello,I., Seidel,D. and Ziegler,A.G.
TITLE	The T-cell receptor beta chain CDR3 region of BV8S1/BV15 transcripts in type 1 diabetes immunogenetics 45 (2), 87-96 (1996)
COMMENT	
FEATURES	
Source	<p>1. .-36 /organism="Mus musculus" /mol_type="mRNA" /strain="BALB/c, F1(BALB/c X C57BL6)" /clone="P25.1.1" /db_xref="taxon:10090" /product="H-2d/Vbeta2b" /haplotype="H-2d/Vbeta2b" /cell_type="CTL clone" /rodent_start=1 /product="T cell receptor beta chain" /protein_id="CDA43155.1" /db_xref="GI:53625" /translation="CASSFOEQYFG" 1..9 /note="Framework branch: FW1" 10..27 /note="Vbeta13/Jbeta2.7 junction" 28..35 /note="Framework branch: FW2" /note="Framework branch: FW2"</p>
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Query Match	66.0%; Score 13.2; DB 6; Length 36;
Best Local Similarity	83.3%; Pred. No. 7.6e+05; Mismatches 3; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3 TTAGGCCACCAAGTGTCAA 20
Db	1 TGTCGCCAGCAGTGACCAA 18
RESULT 13	HSTRK3X32
LOCUS	HSTRK3X32
DEFINITION	H.sapiens mRNA for T cell receptor beta chain junctional region (clone K3-32).
ACCESSION	Z6994
VERSION	Z6994.1
KEYWORDS	GI:1770615
SOURCE	
ORGANISM	Mammalia; Butharia; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	(bases 1 to 39)
AUTHORS	The T-cell receptor beta chain CDR3 region of BV8S1/BV15 transcripts in type 1 diabetes immunogenetics 45 (2), 87-96 (1996)
TITLE	
JOURNAL	
PUBLISHED	8952958

REFERENCE 2 (bases 1 to 39)
 AUTHORS Naberk, H.E.
 TITLE Direct Submission
 JOURNAL Submitted (02-PER-1996) Naserke H.E., Diabetes Research Institute,
 Koenner Platz 1, D-80804 Muenchen, FRG
 FEATURES location/Qualifiers
 source 1..39
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /isolate="type 1 diabetic patient PS"
 /db_xref="taxon:9606"
 /clone="X3-12"
 /cell_type="lymphocytes"
 /tissue_type="peripheral blood"
 /note="HLA type: HLA-A31, 1; Cw3, 3; B62, 55; DRB1*1301,
 DPB1*, 01; DPB1*0301, 0201"
 gene 1..12
 /gene="V beta 8.1"
 v_segment 1..12
 /gene="V beta 8.1"
 N_region 13..17
 /gene="V beta 8.1"
 gene 18..20
 /gene="D beta 2.1"
 D_segment 18..20
 /gene="D beta 2.1"
 gene 21..39
 /gene="J beta 1.5"
 J_segment 21..39
 /gene="J beta 1.5"
 ORIGIN
 Query Match 66.0%; Score 13.2; DB 5; Length 39;
 Best Local Similarity 83.3%; Pred. No. 7.5e+05; Mismatches 3; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 TAGGCCACAGGTCCAA 20
 Db 1 TGTGCCACAGTGCCCAA 18

RESULT 14
 AX55817/c
 LOCUS AX55817
 DEFINITION Sequence 413 from Patent WO202070755.
 ACCESSION AX55817
 VERSION AX55817.1
 KEYWORDS SOURCE
 ORGANISM synthetic construct
 SYNTHETIC CONSTRUCT
 REFERENCE other sequences, artificial sequences.
 AUTHORS Lyamichev, V.I., Kaiser, M.W. and Lyamichova, N.
 TITLE Patent: WO 202070755-A 413 12-SEP-2002;
 JOURNAL Third Wave Technologies, Inc. (US)
 FEATURES FEATURES
 source 1..42
 /organism="Synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 ORIGIN
 Query Match 66.0%; Score 13.2; DB 2; Length 42;
 Best Local Similarity 83.3%; Pred. No. 7.4e+05; Mismatches 3; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 TAGGCCACAGGTCCAA 20
 Db 31 TGTGCCACAGTGCCCAA 14

ORIGIN
 Query Match 66.0%; Score 13.2; DB 5; Length 48;
 Best Local Similarity 83.3%; Pred. No. 7.2e+05; Mismatches 3; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 TAGGCCACAGGTCCAA 20
 Db 1 TGTGCCACAGTGCCCAA 18

SEARCH INFORMATION
 Search completed: May 21, 2006, 22:09:05
 Job time : 103.5 SECs

HSA305425
 Locus HSA305425
 Definition Homo Sapiens partial TCRBV15J2S2 gene for T-cell receptor beta chain, Junctional region, patient I CA, clone #18.
 Accession AJ305425
 Version AJ305425.1 GI:11322060
 Keywords Junctional region; T-cell receptor beta chain; TCR beta chain;
 Source TCRBV15J2S2 gene, variable region.
 Organism Homo Sapiens (human)

REFERENCE 1
 AUTHORS DUCHMANN, R., LAMBERT, C., MAY, B., KOHLER, T. AND MARKER-HERRMANN, E.
 TITLE CD4+ AND CD8+ CLONAL T-CELL EXPANSIONS INDICATE A ROLE OF ANTIGENS IN ANKYLOPSIS SPONDYLITIS; A STUDY IN HLA-B27+ MONOZYGOTIC TWINS
 JOURNAL CLIN. EXP. IMMUNOL. 123 (2), 315-322 (2001)
 PUBLISHED 11207664
 REFERENCE 2 (bases 1 to 48)
 AUTHORS MAY, B.
 TITLE Direct Submission
 JOURNAL Submitted (18-Nov-2000) MAY, B., INTERNAL MEDICINE/RHEUMATOLOGY, UNIVERSITY OF TEXAS SOUTHWESTERN MEDICAL CENTER AT DALLAS, 3523 Harry Hines Blvd, Dallas, TX 75390-8884, USA
 FEATURES FEATURES
 source 1..48
 /organism="Homo Sapiens"
 /mol_type="genomic DNA"
 /isolate="Patient I CA"
 /db_xref="taxon:9606"
 /tissue_type="peripheral blood"
 /genes="TCRBV15J2S2"
 /gene="#18"
 /note="N-D-N joining region (CDR3)"
 /codon_start=1
 /product="T-cell receptor beta chain"
 /protein_id="CXC16912.1"
 /db_xref="GI:11323061"
 /translation="CATSDIGGSTGELFPG"

Om nucleic - nucleic search, using sw model										
Run on: May 21, 2006, 21:34:08 ; Search time 386 Seconds (without alignments) 361.256 Million cell updates/sec										
Title: US-10-766-185-2										
Perfect score: 20										
Scoring table: IDENTITY-NUC Gapopen 10.0 , Gapext 1.0										
Searched: 5244920 seqs, 3486124231 residues										
Total number of hits satisfying chosen parameters: 5218826										
Minimum DB seq length: 0										
Maximum DB seq length: 50										
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries										
Database :										
N_Geneseq_8:*										
1: geneseqn1980s:*										
2: geneseqn1990s:*										
3: geneseqn0008:*										
4: geneseqn2001as:*										
5: geneseqn2001bs:*										
6: geneseqn002as:*										
7: geneseqn2002bs:*										
8: geneseqn2003as:*										
9: geneseqn2003bs:*										
10: geneseqn2003cs:*										
11: geneseqn2003ds:*										
12: geneseqn2004as:*										
13: geneseqn2004bs:*										
14: geneseqn2005as:*										
15: geneseqn2005bs:*										
Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No. Score Query Length DB ID Description										
1	20	100.0	20	13	ADQ88722	Adq88722 Human HIF Adq88722 Human HIF	RESULT 1			
c	20	100.0	20	13	ADQ88721	Adq88721 Human hif	ADQ88722	ID ADQ88722 Standard; DNA; 20 BP.		
3	18.4	92.0	37	2	AAX78996	Aax78996 HIF-1alpha	XX	XX		
4	18	90.0	20	13	ADT88617	Adt88617 HIF1alpha	AC	AC Adq88722;		
c	5	17.4	87.0	19	14	ADZ58028	Adz58028 sense sir	XX	XX	
c	6	17.4	87.0	19	14	ADZ58248	Adz58248 antisense	DT	21-OCT-2004 (first entry)	
c	7	16.4	82.0	32	10	AB203188	Ab203188 toxicolog	XX	XX	
c	8	14.8	74.0	20	14	AEB68623	Aeb68623 mouse glu	PP	28-JAN-2004; 2004US-00766185.	
c	9	14.8	74.0	20	15	AETF79634	Aef79634 mouse glu	PR	31-JAN-2003; 2003US-044367P.	
c	10	14.8	74.0	43	16	ADZ53245	Adz53245 pmp-1 rel	XX		
c	11	14.2	71.0	21	14	ACT45528	Act45528 CDP4 SIRN	DR		
c	12	14.2	71.0	25	2	ADT80533	Adt80533 Pichia pa	XX		
c	13	14.2	71.0	25	2	AAX87554	Aax87554 Pichia pa	PT	New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a	
c	14	14	70.0	20	10	ACPS076	Acps076 Human PRD	PT	nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in	
c	15	14	70.0	24	2	ADG77414	Adg77414 Canine dl	PT	several cancer cells.	
c	16	13.8	69.0	41	3	AAZ59866	Aaz59866 C. elegan	XX		
c	17	13.8	69.0	41	3	AAZ35381	Aaz35381 Omega-3-d	PS	Claim 1; SEQ ID NO 2; 35pp; English.	
c	18	13.6	68.0	29	10	ADK41210	Adk41210 Bndpp Caa	XX		

The invention describes a compound, RX-0047 or RX-0149 targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), where the oligonucleotide compound inhibits the expression of human HIF-1. All described are: a method of inhibiting the expression HIF-1 in human cells or tissues; and a method of inducing cytotoxicity in a cancer cell. Specifically claimed are RX-0047 and RX-0149 compounds having a fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5, aatgagccaccagggtccaa 3', and SEQ ID NO. 4, 5, ggagcttaacatccaaatgc 3', respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The antisense compounds are also useful for preventing or delaying infection, inflammation, or tumour formation. This sequence represents a site on the HIF-1 to which antisense oligonucleotides can be targeted in order to control HIF-1 gene expression.

Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATATGAGCCACCAGGTGTCCAA 20
Db 1 ATATGAGCCACCAGGTGTCCAA 20

RESULT 2
ADQ88721/C
ID ADQ88721 standard; DNA; 20 BP.
XX
AC ADQ88721;
XX DT 21-OCT-2004 (first entry)
XX Human hypoxia inducible factor-1 gene fragment seqid 1.
XX KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; ss.
OS Homo sapiens.
PN US2004152655-A1.
PD 05-AUG-2004.
PP 28-JAN-2004; 2004US-00766185.
XX PR 31-JAN-2003; 2003US-0444367P.
XX PA (YOON/) YOON H.
PA (MAOL/) MAO L.
PA (LIBY/) LIBY Y B.
PA (AHNC/) AHN C.
PA (JIAN/) JIANG X.
PT Voon H, Mao L, Lee YB, Ahn C, Jiang X;
XX DR WPI; 2004-561492/54.
XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in several cancer cells.

PT Disclosure; SEQ ID NO 1; 35pp; English.

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), where the oligonucleotide compound inhibits the expression of human HIF-1. Also described are: a method of inhibiting the expression HIF-1 in human cells or tissues; and a method of inducing cytotoxicity in a cancer cell. Specifically claimed are RX-0047 and RX-0149 compounds having a fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5, aatgagccaccagggtccaa 3', and SEQ ID NO. 4, 5, ggagcttaacatccaaatgc 3',

respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The antisense compounds are also useful for preventing or delaying infection, inflammation, or tumour formation. This sequence represents a site on the HIF-1 to which antisense oligonucleotides can be targeted in order to control HIF-1 gene expression.

Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATATGAGCCACCAGGTGTCCAA 20
Db 20 ATATGAGCCACCAGGTGTCCAA 1

RESULT 3
AX78996
ID AX78996 standard; DNA; 37 BP.
XX AC AX78996;
XX DT 17-AUG-1999 (first entry)
XX DE AX78996
XX KW HIF-1alpha gene amplification primer #2.
XX Chimeric; transactivator protein; DNA binding domain; HIF; VP16; hypoxic-inducible factor; transcriptional activation; expression vector; normoxic; ischaemic tissue; damage; ss.
XX OS Synthetic.
OS Homo sapiens.
XX PN W99928469-A1.
XX PD 10-JUN-1999.
XX PF 04-DEC-1998; 98WO-US025753.
XX PR 04-DEC-1997; 97US-0067546P.
XX PR 13-AUG-1998; 98US-00133612.
XX (GENZ) GENZYME CORP.
XX PT Gregory RJ, Vincent K;
XX DR WPI; 1999-37112/31.
XX Novel nucleic acid encoding a chimeric transactivator.
XX Example 1; Page 74; 81pp; English.

CC The invention relates to a new nucleic acid molecule encoding an active chimeric transactivator protein which comprises (i) the DNA binding domain of a hypoxia-inducible factor protein; and (ii) a protein domain capable of transcriptional activation e.g. the transactivation domain of VP16. The expression vector is used to increase, in a target cell, the expression of a hypoxia-inducible gene. The vector allows sustained expression of active HIF-1α in cells under normoxic conditions and is used for reducing ischaemic tissue damage in a subject having a hypoxia-associated disorder. The primers AX78996-X78996 were used to PCR amplify the full length Hif-1alpha gene for generating the chimeric construct

XX Sequence 37 BP; 13 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 2; Length 37;
Best Local Similarity 95.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATATGAGCCACCAGGTGTCCAA 20

Db 8 AGTGAGGCCACCGTGTCCAA 27
 RESULT 4
 ADT8617 ID ADT8617 standard; DNA; 20 BP.
 AC XX
 DT 27-JAN-2005 (first entry)
 DE HIF1alpha cDNA, antisense oligonucleotide ISIS #298743.
 KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
 KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIFalpha;
 KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
 KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
 KW psoriasis; atherosclerosis; smooth muscle cell proliferation;
 KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
 KW ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;
 KW phosphorothioate; ss.
 OS Homo sapiens.
 OS Mus musculus.
 OS Rattus sp.

XX Key Location/Qualifiers
 PT modified_base 1. -20
 PT /tag= b
 PT /mod_base= OTHER
 PT /note= "Phosphorothioate backbone. All cytidines are 5'-methylcytidine".
 PT modified_base 1. .5
 PT /tag= a
 PT /mod_base= OTHER
 PT /note= "2',-O-Methoxyethyl (2'-MOE) nucleotides"
 PT modified_base 16. -.20
 PT /tag= C
 PT /mod_base= OTHER
 PT /note= "2',-O-Methoxyethyl (2'-MOE) nucleotides"
 PN us2604270393-A1.
 XX PD 04-NOV-2004.
 XX PR 21-NOV-2003; 2003US-00719370.
 XX PR 23-NOV-2002; 2002US-00304126.
 XX PA (WARD/) WARD D T.
 PA (DOB/) DOBIE K W.
 PA (MARC/) MARCUSSEN E G.
 PA (FREI/) FREIER S M.
 XX PI Ward DT, Dobie KW, Marcusson EG, Preier SM;
 DR XX WPI; 2004-774955/76.
 XX PT New antisense compound which inhibits the expression of hypoxia-inducible factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
 XX PS Claim 27; SEQ ID NO 187; 195pp; English.
 XX CC The present invention relates to antisense compounds targeted to nucleic acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound comprises an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits the expression of HIF1alpha and/or HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, preferably a phosphorothioate linkage. It also comprises at least one modified sugar moiety, preferably a 2'-O-

CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further comprises at least one modified nucleobase, preferably a 5'-methylcytosine. The antisense oligonucleotides are useful for the treatment of diseases such as hyperproliferative disorders, e.g. cancer, preferably a cancer carrying a p53 mutation, or an angiogenic disorder that affects the eye. The compound is also useful for treating tumours, hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis, atherosclerosis and smooth muscle cell proliferation in the blood vessels such as stenosis or restenosis following angioplasty. It is also useful in drug discovery and target validation, and can be utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits.

CC The present sequence represents an antisense oligonucleotide used in the examples of the present invention.

CC Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

SQ Query Match 90.0%; Score 18; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TGAGGCCACCGTGTCCAA 20
 ||||||| ||||| ||||| |||||
 ||||| TGAGGCCACCGTGTCCAA 18)

RESULT 5
 AD258028/c
 ID AD258028 standard; RNA; 19 BP.
 XX AC AD258028;
 XX DT 30-JUN-2005 (first entry)
 XX DE Sense siRNA oligo that modulates human HIF1 expression Seq 156.
 XX SS: short interfering RNA; siRNA; gene silencing; RNA interference;
 KW hypoxia inducible factor 1; cancer; hyperproliferation;
 KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
 KW antidiabetic.
 XX OS Homo sapiens.
 PN WO2005035759-A2.
 XX PD 21-APR-2005.
 XX PR 20-AUG-2004; 2004WO-US027224.
 XX PR 20-AUG-2003; 2003US-0496655P.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 10-FEB-2004; 2004US-0543480P.
 PR 13-FEB-2004; 2004US-00780477.
 PR 16-APR-2004; 2004US-00826566.
 PR 30-APR-2004; 54US-0997777.
 PR 24-MAY-2004; 54US-0996666.
 XX PA (SIRNA) SIRNA THERAPEUTICS INC.
 XX PI Usman N, McSwiggen J;
 DR WPI; 2005-306364/31.
 XX PT New chemically synthesized double stranded short interfering nucleic acid molecule that directs cleavage of a hypoxia inducible factor 1 RNA via RNA interference (RNAi), useful for modulating HIF1, its expression or activity.
 XX RS Claim 33; SEQ ID NO 156; 189pp; English.
 XX CC This invention relates to a novel chemically synthesized double stranded

CC short interfering nucleic acid strand (siRNA). Specifically, it refers to to
 CC siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
 CC RNA interference (RNAi). In particular, the siRNA may include short
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1
 CC RNA or a portion thereof, and where a second strand is the complementary
 CC antisense siRNA strand. Note that the sense region is connected to the
 CC antisense region via a polynucleotide linker molecule. Accordingly, these
 CC siRNAs are useful in providing compositions for the treatment of traits,
 CC diseases and conditions that respond to modulation of HIF1 expression,
 CC namely cancer and proliferative conditions including macular
 CC degeneration, diabetic retinopathy and other conditions associated with
 CC hypoxia inducible proliferation. As such, these compositions exhibit
 CC cytostatic, ophthalmological and antidiabetic activities. This
 CC oligonucleotide sequence is a sense siRNA strand that targets human HIF1
 CC RNA to modulate expression given in an exemplification of the invention.
 XX Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
 SQ Query Match 87.0%; Score 17.4; DB 14; Length 19;
 Best Local Similarity 94.7%; Pred. No. 49;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY QY 1 ATATGAGGCCACCGAGTCCA 19
 Db 19 AGTGAAGCCACCAAGTCTCA 1
 AC
 XX RESULT 6
 AD258248 ID AD258248 standard; RNA; 19 BP.
 XX
 AC AD258248;
 XX DT 30-JUN-2005 (first entry)
 XX DB Antisense siRNA oligo that modulates human HIF1 expression seq 376.
 XX KW ss; short interfering RNA; siRNA; gene silencing; RNA interference;
 KW hypoxia inducible factor 1; cancer; hyperproliferation;
 KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
 KW antidiabetic; antisense.
 OS Homo sapiens.
 XX PN WO2005035719-A2.
 XX PD 21-APR-2005.
 XX PP 20-AUG-2004; 2004WO-US027294.
 XX PR 20-AUG-2003; 2003US-0496655P.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 10-FEB-2004; 2004US-007434802.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826956.
 PR 30-APR-2004; 54US-00997777.
 PR 24-MAY-2004; 54US-00996666.
 XX PA (SIRN-) SIRNA THERAPEUTICS INC.
 XX PI Usman N, Moewiggen J;
 XX DR WPI; 2005-306364/31.
 XX PT New chemically synthesized double stranded short interfering nucleic acid
 PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
 PT RNA interference (RNAi), useful for modulating HIF1, its expression or
 PT activity.

PR activity.

XX Claim 33; SEQ ID NO 376; 189pp; English.

XX This invention relates to a novel chemically synthesized double stranded
 CC siRNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
 CC RNA interference (RNAi). In particular, the siRNAs may include short
 CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
 CC and short hairpin RNA (shRNA) molecules that are capable of mediating
 CC siRNA that comprises a nucleotide sequence that is complementary to HIF1
 CC RNA or a portion thereof, and where a second strand is the complementary
 CC antisense siRNA strand. Note that the sense region is connected to the
 CC antisense region via a polynucleotide linker molecule. Accordingly, these
 CC siRNAs are useful in providing compositions for the treatment of traits,
 CC diseases and conditions that respond to modulation of HIF1 expression,
 CC namely cancer and proliferative conditions including macular
 CC degeneration, diabetic retinopathy and other conditions associated with
 CC hypoxia inducible proliferation. As such, these compositions exhibit
 CC cytostatic, ophthalmological and antidiabetic activities. This
 CC oligonucleotide sequence is an antisense siRNA strand that targets human
 CC HIF1 RNA to modulate expression given in an exemplification of the
 CC invention.

XX Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

SQ Query Match 87.0%; Score 17.4; DB 14; Length 19;
 Best Local Similarity 78.9%; Pred. No. 49;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY QY 1 ATATGAGGCCACCAAGTCCA 19
 Db 1 AGTGAAGCCACCAAGTCTCA 19
 AC
 XX RESULT 7
 AD28318/C ID AD28318 standard; DNA; 32 BP.
 XX AC AD28318;
 XX DT 14-MAY-2003 (first entry)
 XX DE Toxicologically relevant human PCR primer #347.
 XX KW Toxicologically relevant gene; toxicological response; PCR primer; BB.
 XX OS Homo sapiens.
 XX OS Synthetic.

XX PN WO200316500-A2.

XX PD 27-FEB-2003.

XX PR 16-AUG-2002; 2002WO-US026514.

XX PR 16-AUG-2001; 2001US-031308P.

XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX PI Neft RB, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
 PI Allen P;
 XX DR WPI; 2003-268322/26.

XX PT determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

XX Claim 1; Page 129; 455pp; English.

CC The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB262842 to AB28764, or their fragments of at least 20 nucleotides, or homologues ; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals

CC Sequence 32 BP; 5 A; 11 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 10; Length 32;
Best Local Similarity 94.4%; **Pred.** No. 1. 7e+02 ; **Matches** 17; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;

QY 1 ATATGAGGCCACCGAGTGTC 18

Db 28 ATGTGAGGCCACCGAGTGTC 11

RESULT 8

ID ARB68623/c
AC ARB68623; ARB68623;
XX 06-OCT-2005 (first entry)

DB Mouse glucocorticoid receptor antisense oligonucleotide SEQ ID NO:243.

KW antisense oligonucleotide; glucocorticoid receptor; antidiabetic; anorectic; diabetes; obesity; syndrome X; hyperglycemia; hyperlipidemia; ss; phosphorothioate; 2'-O-methoxyethyl; 2'-MOR.

OS Mus sp.

XX Key modified_base Location/Qualifiers

PT 1. .20 /*tag= a /mod base= OTHER
PT /note= "phosphorothioate backbone, all cytosine residues are 5'-methylcytosines"
PT 1. .5 /*tag= b /mod base= OTHER
PT /mod bases OTHER
PT /mod bases OTHER
PT /note= "2'-O-methoxyethyl"

PT 16. .20 /*tag= C /mod base= OTHER
PT /note= "2'-O-methoxyethyl"

XX US2005164271-A1.

XX PD 28-JUL-2005.

XX PR 20-JAN-2005; 2005US-00039529.

XX PR 20-JAN-2004; 2004US-0538173P.

PR 03-MAR-2004; 2004US-0550191P.

CC The invention relates to an antisense compound 13-80 nucleobases in length targeted to a nucleic acid molecule encoding glucocorticoid receptor, where the compound is complementary to the nucleic acid molecule encoding glucocorticoid receptor, and where the compound inhibits the expression of glucocorticoid receptor mRNA. Also described: (1) a method of inhibiting the expression of a glucocorticoid receptor in a cell or tissue; (2) a method of treating an animal having a disease or condition associated with glucocorticoid receptor; (3) a method of decreasing blood glucose levels in an animal; and (4) a method of preventing or delaying the onset of an increase in blood lipid levels in an animal. The compounds, compositions, and methods are useful for modulating the expression of glucocorticoid receptor. They are also useful for the diagnosis and treatment of diseases and conditions associated with glucocorticoid receptor, e.g. diabetes (Type 2), obesity, metabolic syndrome X, hyperglycemia, or hyperlipidemia. The present sequence represents a mouse glucocorticoid receptor chimeric phosphorothioate antisense oligonucleotide, which is used in an example from the present invention.

XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; **Pred.** No. 1. 1e+03 ; **Matches** 16; **Conservative** 0; **Mismatches** 2; **Indels** 0; **Gaps** 0;

QY 3 TGAGCCACAGTGTC 20

Db 19 TGACCAACAGGGCCA 2

RESULT 9

ID ARB79634/c
AC ARB79634; ARB79634 standard; DNA; 20 BP.

XX 06-APR-2006 (first entry)

DB Mouse glucocorticoid receptor antisense oligonucleotide, SEQ:243.

KW Antisense therapy; obesity; anorectic; diabetes; antidiabetic; syndrome X; non-insulin dependent diabetes; hyperglycemic; metabolic; glucocorticoid receptor; hypercholesterolemia; anilipemic; metabolic; antisense oligonucleotide; phosphorothioate; ss.

OS Mus musculus.

XX Key modified_base Location/Qualifiers

PT 1. .20 /*tag= a /mod bases OTHER
PT /note= "This oligonucleotide has a phosphorothioate backbone and 2'-methoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytosine residues are 5-methylcytosines"

XX
PN US2006025373-A1.
XX
PD 02-FEB-2005.
XX
PP 18-AUG-2005; 2005US-00207478.
XX
PR 20-JAN-2004; 2004US-0538173P.
PR 03-MAR-2004; 2004US-0530191P.
PR 20-JAN-2005; 2005US-00039629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bhanot S, Doble KW, Freier SM;
XX
DR WPI; 2006-117670/12.
XX
PT New antisense compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding glucocorticoid receptor, useful for treating a disease or condition mediated by glucocorticoid expression, e.g. diabetes, or obesity.
PS Example 13; SEQ ID NO 243; 128pp; English.
CC
The invention relates to antisense oligonucleotides targeted to the glucocorticoid receptor gene, which inhibit its expression. The invention also relates to the use of these antisense oligonucleotides in methods for inhibiting glucocorticoid receptor expression; for reducing blood glucose, triglyceride, cholesterol or insulin levels; for increasing insulin sensitivity; for inhibiting hepatic glucose output; or for reducing body fat mass. The glucocorticoid receptor (encoded on human chromosome 5q11-q13) is a ubiquitously expressed cytoplasmic member of the nuclear hormone superfamily of receptors. It is responsible for mediating the effects of glucocorticoids on various physiological functions e.g., stimulation of gluconeogenesis, decreased glucose uptake and utilization in peripheral tissues, increased glycogen deposition, suppression of immune and inflammatory responses, inhibition of cytokine synthesis, and acceleration of various developmental events. Stress-induced elevation of glucocorticoid synthesis and release can lead to adverse health effects resulting from, amongst other responses, increased ventricular workload, inhibition of inflammatory mediators, inhibition of cytokine synthesis and increased glucose uptake. Cytokine receptor expression may therefore be useful in the treatment of diseases resulting from glucocorticoid activity. Antisense oligonucleotides targeted to the glucocorticoid receptor gene are useful for the treatment of obesity, diabetes (particularly type 2 diabetes), metabolic syndrome X, hyperglycemia and hyperlipidemia (especially elevated blood cholesterol or triglyceride levels). The present sequence represents a phosphorothioate antisense oligonucleotide targeted to mouse glucocorticoid receptor RNA.
SQ Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 15; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.1e+03; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 3 TAGGACGAGTGTCCAA 20
Db 19 TGACCACTGGTCCCCAA 2
RESULT 10
ADE5345/C
ID ADE5345 Standard; DNA; 43 BP.
XX
AC ADE5345;
XX
DT 29-JAN-2004 (first entry)
XX
DB PEN-1 related DNA used within the scope of the invention, #379.
XX
KW Plap endonuclease-1; PEn-1; endonuclease; structure-specific nuclease;
XX
OS Methanocaldococcus jannaschii.
PN WO200270755-A2.
XX
PR 15-NOV-2000; 2000US-00713601.
PR 17-NOV-2000; 2000US-00714935.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev VI, Kaiser MW, Lyamicheva N;
XX
DR WPI; 2002-750464/81.
XX
PT New composition useful for detecting and characterizing nucleic acid sequences and sequence variants for detecting the presence of viral or bacterial infections or cancer, comprises purified or chemical PEn-1 endonuclease.
XX
Example 65; SEQ ID NO 427; 871pp; English.
CC
The invention discloses a new composition (I) which comprises a purified flap endonuclease-1 (PEn-1), from e.g. Sulfolobus solfataricus, Pyrococcus abyssi or a chimerical PEn-1 endonuclease having a portion of the above endonuclease in addition to that of Pyrococcus horikoshii and beropyrum pernix. Also claimed is a composition comprising an isolated nucleic acid sequence encoding the endonuclease mentioned above, a composition comprising a vector having the nucleic acid sequence cited above, a composition comprising a host cell and vector cited above, a mixture comprising a first structure-specific nuclease selected from the species mentioned in composition (I), and a purified second structure-specific nuclease and detecting a target sequence, comprising: (a) providing a sample suspected of containing the target sequence, (b) oligonucleotides capable of forming an invasive cleavage structure in the presence of the target sequence, and a PEn-1 endonuclease selected from the species cited above and (b) exposing the sample to the oligonucleotides and PEn-1 endonuclease. The second structure-specific nuclease also comprises a thermostable DNA polymerase. It has a 5', nucleic acid derived from a DNA polymerase altered in amino acid sequence such that it exhibits reduced DNA synthetic activity from that of the wild-type DNA polymerase but retains substantially the same 5' nucleic acid activity of the wild-type DNA polymerase. The second structure is selected from CLEAVASE BN enzyme, CLEAVASE DA enzyme, CLEAVASE DN enzyme, CLEAVASE DV enzyme, CLEAVASE BN/thrombin enzyme, CLEAVASE TTBDN enzyme, T. aquaticus DNA polymerase, T. thermophilus DNA polymerase, E. coli Exo III and S. cerevisiae Radi/Radio complex. The nucleic acid treatment kit comprises (1) and oligonucleotides capable of forming an invasive cleavage structure in the presence of a target nucleic acid. The oligonucleotides comprise: (a) a first oligonucleotide having a 5' portion complementary to a first portion of a target nucleic acid and (b) a second oligonucleotide comprising a 5' portion complementary to a second portion of the target nucleic acid downstream of and contiguous to the first portion and a 3' portion. The 3' portion of the second oligonucleotide comprises a single 3' terminal nucleotide not complementary to the target nucleic acid. Additionally, the kit has a third oligonucleotide complementary to a third portion of the target nucleic acid upstream of the first portion of the first target nucleic acid. In detecting a target sequence, the oligonucleotides and endonuclease are mixed under conditions where an invasive cleavage structure is formed between the target sequence and the oligonucleotides if the target sequence is present in the sample, where the invasive cleavage structure is cleaved by the endonuclease to form a cleavage product. The composition is useful in detecting and characterising specific nucleic acid sequences and sequence variants which can be used in detecting the presence of viral or bacterial infections, and other diseases such as cancer. The composition may also be used in forensic

CC analysis or for paternity determinations. The sequence presented is a FEN
 CC -1 related DNA used within the scope of the invention.
 XX Sequence 43 BP; 12 A; 13 C; 6 G; 12 T; 0 U; 0 Other;
 SQ

Query Match 74.0%; Score 14.8; DB 6; Length 43;
 Best Local Similarity 88.9%; Pred. No. 1.2e+03; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGCCACCATGTCATA 20
 DB 32 TGAGCCACCATGTCATA 15

RESULT 11
 ACU45528/c
 ID ACU45528 standard; RNA; 21 BP.
 XX
 AC ACU45528;
 XX DT 24-MAR-2005 (first entry)
 DE CDH6 siRNA antisense sequence, SEQ ID 6600.
 KW Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
 KW short interfering RNA; gene silencing.
 OS Synthetic.
 XX PN WO200501092-A2.
 XX PD 06-JAN-2005.
 XX PP 19-MAY-2004; 2004WO-US015645.
 PR 20-MAY-2003; 2003US-0471729P.
 PR (AMHP) WYETH.
 PI Be X, Wei L, Slonim DK, Howes SH;
 DR XX
 XX WPI; 2005-075568/08.

PT pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for treating cancer.
 PT XX
 PS Claim 3; SEQ ID NO 6600; 113pp; English.
 XX
 CC The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNL1D, CDH6, CST, ENPP3, F11l1856, GPR54, HAVCR1, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pct_sequences

XX Sequence 21 BP; 5 A; 4 C; 7 G; 0 T; 5 U; 0 Other;
 SQ

Query Match 71.0%; Score 14.2; DB 14; Length 21;
 Best Local Similarity 84.2%; Pred. No. 2.3e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB

RESULT 13
 AXB87554/c
 ID AXB87554 standard; DNA; 25 BP.
 XX
 AC AXB87554;
 XX DT 08-OCT-1999 (first entry)
 XX DB Pichia pastoris alcohol oxidase PCR primer.

RESULT 12
 ATB80533/c
 ID ATB80533 standard; DNA; 25 BP.
 XX
 AC ATB80533;
 XX DT 25-MAR-2003 (revised)
 DT 04-NOV-1997 (first entry)
 XX Pichia pastoris genomic DNA PCR primer.
 XX KW Isozymes; genomic clone; methanol-regulated promoter; yeast; starch; ethanol; regulatory region; polymerase chain reaction; ss.
 OS Synthetic.
 XX PN US5641661-A.
 XX PD 24-JUN-1997.
 XX PF 25-MAR-1994; 94US-00220506.
 XX PR 25-MAR-1993; 93US-00037617.
 PR 25-MAR-1993; 93US-00037618.
 XX PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX PT Sverlow GG, Kumagai MH;
 XX DR WPI; 1997-340945/31.
 XX PT conversion of starch to ethanol using recombinant yeast - which contain starch-degrading enzyme coding sequence under the control of Pichia ZA1 promoter.
 XX RS Example 6; Col 17; 46pp; English.
 XX
 CC A novel method has been produced for converting starch to ethanol. The method involves growing yeast cells in a culture medium, where the yeast cells contain a genetic construct comprising a nucleotide sequence encoding a starch-degrading enzyme under the control of a ZA1 promoter (the promoter of a Pichia pastoris alcohol oxidase gene). The present sequence represents a PCR primer used in the amplification of Pichia pastoris genomic DNA. The ZA1 promoter can direct high-level expression of the rice alpha-amylase gene in *Saccharomyces cerevisiae*. (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 71.0%; Score 14.2; DB 2; Length 25;
 Best Local Similarity 84.2%; Pred. No. 2.3e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ATGAGGCCACCATGTCATA 20
 DB 19 ATGAGGCCACCATGTCATA 1

KW Gene function; protein function; alcohol oxidase; PCR; primer; AOX1 gene;
 KW ss.
 XX
 OS Synthetic.
 OS *Pichia pastoris.*
 PN WO936516-A2.
 XX
 PD 22-JUL-1999.
 XX
 PP 15-JAN-1999; 99WO-US001164.
 XX
 PR 16-JAN-1998; 98US-00008186.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Della-Cioppa G, Erwin RL, Fitzmaurice WP, Hanley KM, Kumagai MH;
 PI Lindbo JA, Mcgee DR, Padgett HS, Pogue GP;
 XX
 DR WPI; 1999-458459/38.
 XX
 PT Determining the function of polynucleotide sequences and their encoded
 PT proteins by transfecting them into a host organism.
 XX
 PS Example 8, Page 57; 15pp; English.
 CC This primer corresponds to the nucleotide sequence of the *Pichia pastoris*
 CC alcohol oxidase AOX1 gene promoter. It was used in the PCR amplification
 CC of *P. pastoris* cDNA. Expression in transfected *Nicotiana benthamiana*
 CC plants confirmed that the yeast cDNA encoded alcohol oxidase. The
 CC invention provides methods for rapidly determining the function of
 CC nucleic acid sequences by transfecting them into a host organism to
 CC effect expression, and analysing the resulting phenotypic and biochemical
 CC changes. Method for silencing endogenous genes; for selecting desired
 CC functions of RNAs and proteins, and for inhibiting an endogenous protease
 CC in a plant host are also provided.
 XX
 SQ Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 2; Length 25;
 Best Local Similarity 84.2%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 OY 2 ATGAGCCACCGATGCCAA 20
 Db 19 ATGAGCCACCGATGCCAA 1
 RESULT 14
 AC/P58076/C
 ID ACP58076 standard; DNA; 20 BP.
 XX
 AC ACP58076;
 AC
 DT 15-JAN-2004 (first entry)
 XX
 DE Canine disease marker-related PCR primer 258.
 XX
 KW genetic disease; genetic trait; dog; carrier of recessive disease;
 KW copper toxicosis; CT; canine genome map; breed-specific profile;
 KW DNA fingerprint; dog identification; PCR; primer; ss.
 OS Canis familiaris.
 XX
 PN WO9731011-A1.
 XX
 PD 28-AUG-1997.
 XX
 PR 18-FEB-1997; 97WO-US002396.
 XX
 PR 22-FEB-1996; 96US-0012060P.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 DB Human PRDX3 gene fragment C ChIP analysis 5' primer.
 KW PRDX3; tumour; paroxiredoxin 3; cytostatic; gene therapy; ChIP analysis;
 KW chromatin immunoprecipitation; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087312-A2.
 XX
 PD 23-OCT-2003.
 XX
 PR 08-APR-2003; 2003WO-US010539.
 XX
 PR 08-APR-2002; 2002US-0370873P.
 XX
 PA (UWYO) UNIV JOHN HOPKINS.

PI Dang CV, Wansey D;
 XX
 DR WPI; 2003-845314/78.
 XX
 PT Inhibiting tumor growth by delivering to a tumor cell, expressing an mRNA
 PT molecule complementary to native Peroxiredoxin 3 (PRDX3) mRNA, an
 PT antisense construct comprising 15 or 19 nucleotides of a murine or human
 PT PRDX3 cDNA.
 XX
 PS Claim 24; Page 23; 0PP; English.
 XX
 CC The invention relates to inhibiting tumour growth. The method involves
 CC delivering to a tumour cell an antisense construct comprising at least 15
 CC or 19 nucleotides of a murine or human Peroxiredoxin 3 (PRDX3) cDNA,
 CC where the tumour cell expresses an mRNA molecule that is complementary to
 CC native PRDX3 mRNA. The method is useful for inhibiting tumour growth.
 CC Sequences ACP58074-91 represent primers used in real-time PCR for ChIP
 CC (chromatin immunoprecipitation) analysis of human PRDX3 genomic DNA
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 70.0%; Score 14; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 18 GAGCCACCAAGTGTC 5
 OY 4 GAGCCACCAAGTGTC 17
 RESULT 15
 AC/P58076/C
 ID ACP58076 standard; DNA; 24 BP.
 XX
 AC ACP58076;
 AC
 DT 11-MAR-2004 (first entry)
 XX
 DE Canine disease marker-related PCR primer 258.
 XX
 KW genetic disease; genetic trait; dog; carrier of recessive disease;
 KW copper toxicosis; CT; canine genome map; breed-specific profile;
 KW DNA fingerprint; dog identification; PCR; primer; ss.
 OS Canis familiaris.
 XX
 PN WO9731011-A1.
 XX
 PD 28-AUG-1997.
 XX
 PR 18-FEB-1997; 97WO-US002396.
 XX
 PR 22-FEB-1996; 96US-0012060P.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 DB Human PRDX3 gene fragment C ChIP analysis 5' primer.
 KW PRDX3; tumour; paroxiredoxin 3; cytostatic; gene therapy; ChIP analysis;
 KW chromatin immunoprecipitation; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087312-A2.
 XX
 PD 23-OCT-2003.
 XX
 PR 08-APR-2003; 2003WO-US010539.
 XX
 PR 08-APR-2002; 2002US-0370873P.
 XX
 PA (UWYO) UNIV JOHN HOPKINS.

PI New oligonucleotide primers for diagnosis of genetic diseases and traits
 PT in dogs - amplify specific regions of the genome containing
 PT microsatellite repeats, especially for diagnosing copper toxicosis and
 PT carrier.
 XX
 PS Claim 1; Page 14; 40pp; English.
 XX
 CC This invention relates to novel oligonucleotide PCR primers which may be
 CC used to identify markers associated with genetic diseases and traits in
 CC dogs, in particular to diagnose genetic diseases that are not
 CC specifically visible and to identify carriers of recessive diseases. A
 CC specific application is diagnosis of copper toxicosis (CT). The invention

CC can also be used to create a genetic map of the canine genome; to
CC generate breed-specific profiles; to establish paternity and to identify
CC dogs from DNA fingerprints. The method provides rapid analysis of the
CC target sequences from only a small sample of DNA. Diagnosis can be done
CC at any time in the dog's life. The present sequence is that of a PCR
CC primer of the invention.

XX Sequence 24 BP; 6 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGCCACGT 14
Db 20 ATGAGGCCACGT 7

Search completed: May 21, 2006, 22:31:24
Job time : 388 secS

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om nucleic - nucleic search, using SW model

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds
(without alignments)
509.284 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20
Sequence: 1 aatggacccagggtccaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqB, 27959665780 residues
Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:

1: gb_est1:
2: gb_est2:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_est7:
7: gb_est8:
8: gb_est9:
9: gb_est10:
10: gb_est11:
11: gb_gb1:
12: gb_gb2:
13: gb_gb3:
14: gb_gb4:
15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1	AU10418/c	
LOCUS	AU10418	50 bp mRNA linear EST 28-JAN-2004
DEFINITION	AU10418 Sugano Homo sapiens cDNA library Homo Sapiens cDNA clone	
ACCESSION	AU10418	HEP2673, mRNA sequence.
VERSION	AU10418.1	GT:13553939
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Boreochondrolires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsumoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Iogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Natamura,Y., Sugama,A. and Sugano,S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	MBO Rep. 2 (5), 388-393 (2001)	
PUBLISHED	1135929	
COMMENT	Contact: Yutaka Suzuki	
	Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Tel: 81-3-5449-5343 Fax: 81-3-5449-5416	
	Email: yuzuki@hgc.jp	
	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Sugama,A. and Sugano,S., Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
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	/db_xref="taxon:9606"	
	/clone="HRP2673"	
	/clone_lib="Sugano Homo sapiens cDNA library"	

Query	Match	68.0%; Score 13.6; DB 1; Length 50;
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Db	35	ATGAGGCCACCGTGTCCA	15	CC571047	CC571047	CH240_446F14	T7	CHORI-240	Bos taurus	genomic	DNA	50 bp	linear	GSS 18-JUN-2003	Best Local Similarity 80.0%; Pred. No. 8.3e+04; Mismatches 4; Indels 0; Gaps 0;
REFERENCE	1	(bases 1 to 50)	1	CC571047	CC571047	CH240_446F14	T7	CHORI-240	Bos taurus	genomic	DNA	50 bp	linear	GSS 18-JUN-2003	Best Local Similarity 80.0%; Pred. No. 8.3e+04; Mismatches 4; Indels 0; Gaps 0;
AUTHORS	Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girin, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mattheison, C., Wye, N., Mason, A., Brown, John, M., Jones, S., Schasin, J., Marras, M., de Jong, P., Keele, J. W. and Kappes, S. M.	1	(bases 1 to 47)	CC571047	CC571047	CH240_446F14	T7	CHORI-240	Bos taurus	genomic	DNA	50 bp	linear	GSS 18-JUN-2003	Best Local Similarity 80.0%; Pred. No. 8.3e+04; Mismatches 4; Indels 0; Gaps 0;
TITLE	Unpublished (2003)	Other GSAs: CH240_446F14.TARBAC13P2	Contract: Rob Holt	Sequencing	The British Columbia Cancer Agency Genome Science Centre	600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6	Tel: 604-877-0855	Fax: 604-877-2276	Email: rholz@cgbc.ca	Copies are derived from the bovine BAC library CHORI-240 available, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering-information.html). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australian and the British Columbia Genome Sciences Centre, Canada. Plate: 446 row: F column: 14 Seq primer: T7 Class: BAC ends.	LOCUS	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.
JOURNAL	COMMENT	Unpublished (2000)	Contact: Robert B. Weiss	University of Utah Genome Center	REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longae, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.									
SOURCE	ORGANISM	Mus musculus (house mouse)	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert	AUTHORS	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Sciurognathi; Muridae; Muridae; Murinae; Mus									
KEYWORDS	KEYWORD	GSS.	JOURNAL	Unpublished (2000)	COMMENT	1 (bases 1 to 47)									
VERSION	VERSION	AZ588937	COMMENT	Unpublished (2000)	CONTACT	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longae, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	1 (bases 1 to 47)									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longae, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	1 (bases 1 to 47)									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longae, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	1 (bases 1 to 47)									
KEYWORDS	KEYWORD	GSS.	COMMENT	Unpublished (2000)	CONTACT	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longae, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.									
FEATURES	FEATURES	High quality sequence stop: 47.	FEATURES	High quality sequence stop: 47.	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
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FEATURES	FEATURES	1. .47	FEATURES	1. .47	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
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source	source	/strain="Breed: Hereford"	source	/strain="Breed: Hereford"	source	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
FEATURES	FEATURES	/sex="Male"	FEATURES	/sex="Male"	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
source	source	/sex="Male"	source	/sex="Male"	source	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
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FEATURES	FEATURES	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"	FEATURES	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
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FEATURES	FEATURES	/sex="Male"	FEATURES	/sex="Male"	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
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FEATURES	FEATURES	ORIGIN	FEATURES	ORIGIN	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
source	source	Query Match 68.0%; Score 13.6; DB 12; Length 50; Best Local Similarity 80.0%; Pred. No. 8.2e+04; Mismatches 4; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 1 ATGAGGCCACCGTGTCCA 20 Db 29 ATGAGGCCACCGTGTCCA 10	FEATURES	Query Match 66.0%; Score 13.2; DB 11; Length 47; Best Local Similarity 83.3%; Pred. No. 1.3e+03; Mismatches 3; Indels 0; Gaps 0; Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0; Qy 2 ATGAGGCCACCGTGTCCA 19 Db 38 ATGAGGCCACCGTGTCCA 21	FEATURES	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						
RESULT	3	RESULT 3	RESULT	RESULT 3	RESULT	AZ588937	IM0397M06R	Mouse 10kb plasmid UGCGM library	Mus musculus genomic clone UGCGIM0397M06 R, genomic survey sequence.						

RESULT 4
LOCUS DY245677 50 bp mRNA linear EST 06-FEB-2006
DEFINITION CSTBD1177A_0_50 CST-BM Mus musculus cDNA, mRNA sequence.
ACCESSION DY245677
VERSION DY245677.1 GI:6581321
KEYWORDS EST.
JOURNAL Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
REFERENCE Sciuromachi, Butcher; Buarachontogires; Glires; Rodentia;
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Muridae; Murinae; Mus.
 1 (bases 1 to 50)
BOWMAN, T.V., McCOOY, A.J., MERCHANT, A.A., RAMOS, C.A., FONSECA, P.,
PONDEXTHER, A., BRADFUTE, S.B., OLIVEIRA, D.M., GREEN, R., ZHENG, Y.,
JACKSON, K.A., CHAMBERS, S.M., MCKINNEY-FREEMAN, S.L., NORWOOD, K.G.,
DARLINGTON, G., GUNARATNE, P.H., STEFFEN, D., AND GOODALE, M.A.
DIFFERENTIAL mRNA Processing in Hematopoietic Stem Cells
Stem Cells (2006) In press
 Contract: Goodale MA
 Center for Cell and Gene Therapy
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713 798 1265
 Fax: 713 798 1230
 Email: goodale@bcm.edu.

FEATURES
source

FEATURES
source

LOCATION/QUALIFIERS
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 /clone_id="CST-BM"
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 /notes="Vector: FWD42nv; Purified genomic DNA from M.
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 Laboratory Mouse DNA Resource (http://wwwjax.org/resources/documents/dnarecs/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The DNA
 adaptored DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G1|4732114gb|AF129072.1), a copy-number
 inducible derivative of Plasmid R1. The vector was ligated
 with adaptor complementary to the insect adaptor and
 purified. The sheared, adaptored mouse DNA was annealed to
 adaptored vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 50;
Best Local Similarity 83.3%; **Pred.** No. 1.3e+05;
Matches 15; **Conservative** 0; **Mismatches** 3; **Indels** 0; **Gaps** 0;

Oy 3 TAGGCCAACAGTCCAA 20
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Db 24 TTAGGCACCGGACAA 7
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RESULT 5
LOCUS AZ601003 19 bp linear GSS 13-DEC-2000
DEFINITION 1M019M06P Mouse 10kb plasmid UGGCM1Mo19M06 F, genomic survey sequence.
ACCESSION AZ601003
VERSION AZ601003.1 GI:11723193
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcher; Buarachontogires; Glires; Rodentia; Eukaryota; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beckorn, T., Duval, B., Hamil, C., Isham, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederauer, A. and Wright, D., Webb, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert

JOURNAL Unpublished (2000)
 Contact: Robert B. Weira
 University of Utah Genome Center

COMMENT

RESULT 6
LOCUS BG389555 46 bp mRNA linear EST 12-MAR-2001
DEFINITION BG389655 mRNA sequence.
ACCESSION BG389655
VERSION BG389655.1 GI:13283103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarachontogires; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1 (bases 1 to 46)
JOURNAL NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Straubberg, Ph.D.
 Email: cgabro@remail.nih.gov
COMMENT Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The T.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>

Plate: LLM10426 row: a column: 01

High quality sequence stop: 46.

FEATURES source

Location/Qualifiers

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/ab_xref="taxon:9606"

/clone="IMAGE:4223400"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC_92"

/notes="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed."

Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC library."

ORIGIN

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 46;

Best Local Similarity 87.5%; Pred. No. 2e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGT 16

3 ACTGGAGCCACCACTAT 18

RESULT 8

CS18330 CL518330 Plunking Sequence Tag of *Oryza sativa* T-DNA insertion lines

DEFINITION DAED11 Plunking Sequence Tag of *Oryza sativa* T-DNA insertion lines

Oryza sativa (Japonica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL518330

VERSION CS18330.1 GI:46145130

GSS: GSS.

SOURCE Oryza sativa (Japonica cultivar-group)

ORGANISM *Oryza sativa* (Japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; ESDP clade; Einhardioideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 49)

AUThORS Sallaud,C., Giv,C., Larmande,P., Bes,M., Piffanelli,P., Piegue,B., Broc,G., Regad,F., Bourgeois,E., Meynard,D., Perrin,C., Gheyskens,A., Deleuze,M., Glaszmann,J.C. and Guiderdoni,E.

TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards *in silico* reverse genetics

JOURNAL TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

COMMENT TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

CONTACT Plant J. (2004) In press

TEl: 33467615629

Fax: 3346761605

Email: emmanuel.guiderdoni@cirad.fr

Class: TDNA tagged.

CIRAD UMR PIA Biotrop program

TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

COMMENT TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

CONTACT Plant J. (2004) In press

TEl: 33467615629

Fax: 3346761605

Email: emmanuel.guiderdoni@cirad.fr

Class: TDNA tagged.

FEATURES source

REFERENCE /organism="Homo sapiens"

LOCUS 602415101P1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4523401

DEFINITION mRNA Sequence.

ACCESSION BG389736

VERSION BG389736.1 GI:13283172

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

COMMENT 1 (bases 1 to 46)

1. NIH_MGC <http://mgc.ncbi.nlm.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: rgs@brrmail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

<http://image.lnl.gov>

Place: LLM10426 row: a column: 02

High quality sequence stop: 46.

Location/Qualifiers

1..46

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4523401"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH_MGC_92"

/notes="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed."

Average insert size 2.5 kb. Library enriched for full-length clones and constructed by life technologies.

Note: this is a NIH_MGC library."

FEATURES source

REFERENCE /organism="Homo sapiens"

LOCUS 602415101P1 NIH_MGC_92

DEFINITION mRNA Sequence.

ACCESSION BG389736

VERSION BG389736.1 GI:13283172

KEYWORDS EST

SOURCE Homo sapiens (human)

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

COMMENT 1 (bases 1 to 46)

1. NIH_MGC <http://mgc.ncbi.nlm.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

ORIGIN

Query Match 63.0%; Score 12.6; DB 13; Length 49;

Best Local Similarity 78.9%; Pred. No. 2.e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 AATGAGCCACCACTGT 19

11 AATAAGCAACCATGATCA 29

RESULT 9

CZ194627/C

LOCUS	CZ194627	35 bp	DNA	linear	GSS 15-AUG-2005	University of Utah Genome Center
DEFINITION	PSI2762-NR MICB1	Mus musculus	genomic	clone	PSI2762-NR, genomic	University of Utah
ACCESSION	CZ194627	survey sequence.				84112, USA
VERSION	CZ194627.1					Tel: 801 585 5606
KEYWORDS	GSS					Fax: 801 585 7177
SOURCE	Mus musculus	(house mouse)				Email: dunn@genetics.utah.edu
ORGANISM	Mus musculus					Insert Length: 10000 Std Err: 0.00
AUTHORS	Hicks,G.G.					Plate: 028 row: E column: 19
JOURNAL	www.Escellig.ca					Seq Primer: CGTGTAGAACGAGCGGT
COMMENT	Unpublished (2002)					Class: Plasmid ends
FEATURES	High quality sequence stop: 38.					
source	Location/Qualifiers					
	1..38					
source	/organism="Mus musculus"					
	/mol_type="genomic DNA"					
	/strain="C57BL/6J"					
	/db_xref="traxon:10050"					
	/clone="UJGCIM0228E19"					
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-					
	/clone_lname="Mouse 10kb plasmid UJGCIM library"					
	/notes="Vector: PWD4Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to purified vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."					
ORIGIN						
Query Match	61.0%	Score 12.2;	DB 13;	Length 35;		
Best Local Similarity	82.4%	Pred. No. 3	9e+05;			
Matches	14;	Conservative	0;	Mismatches	3;	
Qy	2 ATGAGCCACCACTGTC 18			Indels	0;	Gaps 0;
Db	34 ATGGGCCACCACTGCC 18					
RESULT 10						
AZ433336/c	AZ433336	38 bp	DNA	linear	GSS 03-OCT-2000	
DEFINITION	1M0228E19P	Mouse 10kb plasmid UGGIM library	Mus musculus	genomic		
ACCESSION	AZ433336	clone UGGIM0228E19_P, genomic survey sequence.				
VERSION	AZ433336.1	GI:10562349				
KEYWORDS	GSS					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mbo.					
REFERENCE	Dunn,D., Aoyagi,A., Barker,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meelen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhäusern,A. and Wright,D., Weiss,R.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Insert					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss					
RESULT 11						
AI689573	AI689573	40 bp	mRNA	linear	EST 27-MAY-1999	
DEFINITION	txpsh04_x1	NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2277367	3			
ACCESSION	AI689573	similar to SW_0A21_CHICK_P02467 PROCOLLAGEN ALPHA 2(1) CHAIN PRECURSOR ;contains MER22.t3 MSRI repetitive element ;, mRNA sequence.				
VERSION	AI689573					
KEYWORDS	EST.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 40)					
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .					
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
COMMENT	Unpublished (1997)					

FEATURES	source	High quality sequence stop: 1.
source		Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
		cDNA Library Preparation: Life Technologies, Inc.
		cDNA Library Arrayed by: Greg Lennon, Ph.D.
		DNA Sequencing Center found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbprp/image/html
clone distribution:		NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbprp/image/html
Trace considered overall poor quality		Seq primer: -40UP from Gibco
High quality sequence stop: 1.		Location/Qualifiers
Location/Qualifiers		1. . 40
Location/Qualifiers		/organism="Homo sapiens"
Location/Qualifiers		/mol_type="mRNA"
Location/Qualifiers		/db_xref="taxon:9606"
Location/Qualifiers		/clone="IMAGE:227367"
Location/Qualifiers		/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
Location/Qualifiers		/lab_host="DH10B"
Location/Qualifiers		/clone lib="NCI CGAP Ut4"
Location/Qualifiers		/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
ORIGIN		
Query Match		60.0%; Score 12; DB 1; Length 40;
Best Local Similarity		75.0%; Pred. No. 5.e-05;
Matches		15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy		1 ATGAGCCACCACTGTCCAA 20
Db		16 AAGGAGCCAAAGGGTCAA 35
RESULT 12		
AA165872		
LOCUS		AA165872 46 bp mRNA linear EST 19-DEC-1996
DEFINITION		m88b09_r1 Life Tech mouse embryo 13 sdcg 10666014 Mus musculus cDNA clone IMAGE:644777 5', similar to TR:G295543 AFRICAN CLAWED FROG BETA-TSCP. , mRNA sequence.
ACCESSION		AA165872.1
VERSION		EST:1744331
KEYWORDS		Mus musculus (house mouse)
SOURCE		ORGANISM
ORGANISM		Homo sapiens
RESULT 13		
AA165872		
LOCUS		AA165872 49 bp mRNA linear EST 21-DEC-1996
DEFINITION		wj38109.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2405129 3', similar to SW:ACP2_HUMAN P30041 ANTOXIDANT PROTEIN 2 , mRNA sequence.
ACCESSION		AA165872.1
VERSION		EST:1744331
KEYWORDS		Homo sapiens (human)
SOURCE		ORGANISM
ORGANISM		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE		
AUTHORS		1. (bases 1 to 49) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL		Unpublished (1997)
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov
		Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
		cDNA Library Preparation: M. Bento Soares, Ph.D.
		cDNA Library Arrayed by: Greg Lennon, Ph.D.
		DNA Sequencing Center found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbprp/image/html
FEATURES		Trace considered overall poor quality
source		Insert Length: 2063 Std Error: 0.00
Seq primer:		-40UP from Gibco
High quality sequence stop: 1.		Location/Qualifiers
Location/Qualifiers		1. . 49
Location/Qualifiers		/organism="Homo sapiens"
Location/Qualifiers		/mol_type="mRNA"
Location/Qualifiers		/db_xref="taxon:9606"
Location/Qualifiers		/clone="IMAGE:2405129"
Location/Qualifiers		/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
Location/Qualifiers		/dev_stage="adult"
Location/Qualifiers		/lab_host="DH10B (phage-resistant)"
Location/Qualifiers		/clone lib="NCI CGAP Lu19"
Location/Qualifiers		/note="Organ: lung; Vector: pRT3D-Paci; 1st strand cDNA seq primer: -28M13 revl from Amersham
FEATURES		This clone is available royalty-free through LINL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
source		Seq primer: -40UP from Gibco
High quality sequence stop: 1.		Location/Qualifiers
Location/Qualifiers		1. . 49
Location/Qualifiers		/organism="Homo sapiens"
Location/Qualifiers		/mol_type="mRNA"
Location/Qualifiers		/db_xref="taxon:9606"
Location/Qualifiers		/clone="IMAGE:2405129"
Location/Qualifiers		/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
Location/Qualifiers		/dev_stage="adult"
Location/Qualifiers		/lab_host="DH10B (phage-resistant)"
Location/Qualifiers		/clone lib="NCI CGAP Lu19"
Location/Qualifiers		/note="Organ: lung; Vector: pRT3D-Paci; 1st strand cDNA seq primer: -28M13 revl from Amersham

was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR/3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo.

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.2e+05; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CACCAAGTGTCGA 19
Db 24 CACCAAGTGTCGA 13

RESULT 14

CW213788/c

DEFINITION CW213788 50 bp DNA linear GSS 31-OCT-2004
LOCUS 104 746_11404087_148_35356_024_Sorghum methylation filtered library
(LIBID: 104) Sorghum_bicolor genomic clone 11404087, genomic survey sequence.

ACCESSION CW213788

VERSION CW213788.1

KEYWORDS GI:54989976

SOURCE GSS

ORGANISM Sorghum bicolor (sorghum)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 50)

AUTHORS Bedell,J.A., Budiman,M.A., Nurnberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,B., Rohlfing,T., Fries,J., Bradford,K., Korf,I.F., McManamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and Marlienssen,R.A.

Sorghum genome sequencing by methylation filtration PROS Biol. 3(1), e13 (2005) 15660154

COMMENT Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 746 row: 1 column: 07

Seq primer: sf09 Forward

Clas: methylation filtered

High quality sequence stop: 50.

FEATURES Source
FEATURES Source
1. .50
/organism="Sorghum bicolor"
/mol_type="Genomic DNA"
/cultivar="ATCC23"
/db_xref="taxon:4558"
/clone="11404087"
/clone_lib="Sorghum methylation filtered library (libid: 104); /note="Organ: leaf; Vector: pBCK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN
Query Match 60.0%; Score 12; DB 13; Length 50;
Best Local Similarity 75.0%; Pred. No. 5.2e+05; Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGAGGCCACGTG 15
Db 2 ATGACGCCACATG 16

Db 31 AGTGAGCTTACACTCTGCAA 12

DEFINITION Yb7109_r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:76655 5, Similar to similar to gb:X16869 ELONGATION FACTOR 1-ALPHA 1 (HUMAN), mRNA sequence.

ACCESSION T51051

VERSION T51051.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 30)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., Dubroff,T., Faville,A., Gish,W., Hawkins,M., Holtzman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.

COMMENT Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 575

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LUMI, This clone is available royalty-free through LUMI; contact the IMAGE Consortium (info@image.lnl.gov)

Insert Length: 576 Std Error: 0.00

Seq Primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1..30

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:506314"

/db_xref="taxon:9606"

/clone="IMAGE:76625"

/sex="female"

/dev_stage="49 year old"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Stratagene ovary (#937217)"

/note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo dT.

Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTGGCGAGGAG 3', -3' adaptor sequence: 5'; TCCTGGTTTTTTTTTTTTT 3',

ORIGIN

Query Match 59.0%; Score 11.8; DB 10; Length 30;

Best Local Similarity 86.7%; Pred. No. 6.1e+05; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGGCCACGTG 15

Db 2 ATGACGCCACATG 16

Mon May 22 14:33:49 2006

us-10-766-185-2.rbt

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: May 21, 2006, 22:08:44 ; Search time 115.5 Seconds

(without alignments)
324.002 Million cell updates/sec

Title: US-10-766-185-2
Perfect score: 20
Sequence: 1 aatgagccaccagtgtccaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1-COMB.seq: *
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5-COMB.seq: *
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A-COMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B-COMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7-COMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H-COMB.seq: *
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS-COMB.seq: *
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP-COMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE-COMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfilesl.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result: Maximum Match 100%
Listed first 45 summaries

No.	Score	Query Length	DB ID	Description
1	18.4	92.0	37	US-09-579-897-2 Sequence 2, Appl1
2	14.2	71.0	25	US-08-220-606B-13 Sequence 13, Appl1
3	14	70.0	25	US-09-390-196G-97802 Sequence 97802, A
4	14	70.0	25	US-09-390-196G-97803 Sequence 97803, A
5	14	70.0	25	US-09-396-196G-97804 Sequence 97804, A
6	14	70.0	25	US-09-396-196G-97805 Sequence 97805, A
7	13.8	69.0	41	US-09-330-231-3 Sequence 3, Appl1
8	13.4	67.0	25	US-09-336-196G-99591 Sequence 99591, A
9	13.4	67.0	25	US-09-336-196G-99592 Sequence 99592, A
10	13.4	67.0	25	US-09-336-196G-99593 Sequence 99593, A
11	13.2	66.0	20	US-09-601-755-66 Sequence 66, Appl1
12	13.2	66.0	22	US-09-216-398B-208 Sequence 208, Appl1
13	13.2	66.0	25	US-09-396-196G-60300 Sequence 60900, A
14	13.2	66.0	25	US-09-396-196G-60301 Sequence 60901, A
15	13.2	66.0	50	US-10-131-827-6025 Sequence 6025, Appl1
16	13.2	66.0	50	US-10-131-831-6025 Sequence 6025, Appl1
17	13	65.0	25	US-09-336-196G-97819 Sequence 97819, A
18	12.8	64.0	20	US-10-131-827-9040 Sequence 9040, Appl1
19	12.8	64.0	25	US-09-336-196G-95033 Sequence 50633, A
20	12.8	64.0	25	US-09-336-196G-57705 Sequence 57705, A
21	12.8	64.0	25	US-09-336-196G-114077 Sequence 114077, A
22	12.8	64.0	25	US-09-336-196G-114078 Sequence 114078, A
23	12.8	64.0	3	US-09-396-196G-114079 Sequence 114079, A

ALIGNMENTS

SEQ ID NO	TYPE: DNA	LENGTH: 37	SEQUENCE
1	ORGANISM: Homo sapiens		US-09-579-897-2
2			aatgagccaccagtgtccaa 20
3			AATGAGCCACCAGTGTCCAA 20
4			AATGAGCCACCAGTGTCCAA 27
5			AATGAGCCACCAGTGTCCAA 27
6			AATGAGCCACCAGTGTCCAA 27
7			AATGAGCCACCAGTGTCCAA 27
8			AATGAGCCACCAGTGTCCAA 27
9			AATGAGCCACCAGTGTCCAA 27
10			AATGAGCCACCAGTGTCCAA 27
11			AATGAGCCACCAGTGTCCAA 27
12			AATGAGCCACCAGTGTCCAA 27
13			AATGAGCCACCAGTGTCCAA 27
14			AATGAGCCACCAGTGTCCAA 27
15			AATGAGCCACCAGTGTCCAA 27
16			AATGAGCCACCAGTGTCCAA 27
17			AATGAGCCACCAGTGTCCAA 27
18			AATGAGCCACCAGTGTCCAA 27
19			AATGAGCCACCAGTGTCCAA 27
20			AATGAGCCACCAGTGTCCAA 27
21			AATGAGCCACCAGTGTCCAA 27
22			AATGAGCCACCAGTGTCCAA 27
23			AATGAGCCACCAGTGTCCAA 27

RESULT 2
US-08-220-606B-13/C
; Sequence 13, Application US/08220606B
; Patient No. 5561661
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: Genaidi, Sverlow J.
; TITLE OF INVENTION: Pichia Pastoris Alcohol Oxidase Zzal and
; TITLE OF INVENTION: Zza2 Regulatory Regions for Heterologous Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10016

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentRelease #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/220,606B
 FILING DATE: 25-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 8129-065

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEX: 66141 PENNIE
 TELFAX: 415-854-3694

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA
 US-08-220-606B-13

Query Match 71.0%; Score 14.2; DB 2; Length 25;
 Best Local Similarity 84.2%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ATGAGCCACCAAGTCCA 20
 Db 19 ATGAGCCACACAGTCGA 1

RESULT 3
 Sequence 97802, Application US/09396196G
 ; Sequence 97802, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: PatSeq for Windows Version 4.0
 ; SEQ ID NO: 97804
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mmu musculus
 ; US-09-396-196G-97802

Query Match 70.0%; Score 14; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCACCAAGTGCTCA 19
 Db 25 GCACCAAGTGCTCA 12

RESULT 4
 Sequence 97803, Application US/09396196G
 ; Sequence 97803, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: PatSeq for Windows Version 4.0
 ; SEQ ID NO: 97803
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mmu musculus
 ; US-09-396-196G-97803

RESULT 5
 Sequence 97804, Application US/09396196G
 ; Sequence 97804, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: PatSeq for Windows Version 4.0
 ; SEQ ID NO: 97804
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mmu musculus
 ; US-09-396-196G-97804

Query Match 70.0%; Score 14; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCACCAAGTGCTCA 19
 Db 22 GCACCAAGTGCTCA 9

RESULT 6
 Sequence 97805, Application US/09396196G
 ; Sequence 97805, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis

```

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/000,678
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO: 97805
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-97805

Query Match 70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GGCAACAGGTGCTCA 19
Db 20 GCCACCAAGTGCTCA 7

RESULT 7
US-09-330-235-3/c
Sequence 3, Application US/09330235
Patient No. 6459018
GENERAL INFORMATION:
APPLICANT: Kutzon, Debbie
TITLE OF INVENTION: POLYNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: MOCO.156.000S
CURRENT APPLICATION NUMBER: US/09/330,235
PRIORITY FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 41
TYPE: DNA
ORGANISM: Synthetic primer
US-09-330-235-3

Query Match 69.0%; Score 13.8; DB 3; Length 41;
Best Local Similarity 88.2%; Pred. No. 9.3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAGGCCACCGTGTCTC 17
Db 34 ATGGAGCCACCATGTGTC 18

RESULT 8
US-09-396-196G-99591
Sequence 99591, Application US/09396196G
Patient No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 99591
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-99591

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 AGCCACAGGTGCTCA 19
Db 11 AGCCCCAGTGCTCA 25

RESULT 9
US-09-396-196G-99592
Sequence 99592, Application US/09396196G
Patient No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
PRIORITY FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 99592
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-99592

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 AGCCACAGGTGCTCA 19
Db 11 AGCCCCAGTGCTCA 25

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RESULT 11
US-09-661-753-6/C
; Sequence 66, Application US/09661753
; Patent No. 6416909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; PRIORITY FILING DATE: 1999-09-17
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: 
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-661-753-66

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 3; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ATGAGCCACAGGTCCA 19
Db 19 ATGAGCTTACCTGGTCCA 2

RESULT 12
US-09-216-393B-208/C
; Sequence 208, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIORITY FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: 
; OTHER INFORMATION: Synthetic Primer
; US-09-216-393B-208

Query Match
Best Local Similarity 83.3%; Score 13.2; DB 3; Length 22;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ATGAGCCACAGGTCCA 19
Db 21 ATGAGCTTACCTGGTCCA 4

RESULT 13
US-09-396-196G-60900
; Sequence 15, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PATSEQ for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-60901

Query Match
Best Local Similarity 83.3%; Score 13.2; DB 3; Length 25;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ATGAGCCACAGGTCCA 19
Db 2 ATGAGCTTACCTGGTCCA 19
Db 5 ATGAGCTTACCTGGTCCA 22

RESULT 14
US-09-396-196G-60901
; Sequence 60901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PATSEQ for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-60901

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 3; Length 25;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ATGAGCCACAGGTCCA 19
Db 2 ATGAGCTTACCTGGTCCA 19
Db 2 ATGAGCTTACCTGGTCCA 19

RESULT 15
US-10-131-827-6025/C
; Sequence 6025, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-05
; PRIORITY FILING DATE: 2001-10-22
; PRIORITY APPLICATION NUMBER: US 10/006,290
; PRIORITY FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
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; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 6025
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6025

Query Match 66.0%; Score 13.2; DB 3; Length 50;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	3	TGAGGCCACCACTGTCCA 20
Db	22	TGAAACACCACTGTACCAA 5

Search completed: May 21, 2006, 23:25:18
Job time : 116.5 secs

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OM nucleic - nucleic search, using SW model

Run on: May 21, 2006, 22:09:18 ; Search time 654 Seconds
 (Without alignments)
 375.769 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 atatggccaccatgttccaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:

24111450

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match of 4

Listing first 45 summaries

Database : Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11E_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. Score Query NO. Match Length DB ID Description

ALIGNMENTS

18	14.8	74.0	25	8	US-10-719-956-517759	Sequence 517759,	
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c	20	14.8	25	9	US-10-719-900-852952	Sequence 41993,	
c	21	14.8	25	9	US-10-719-900-852952	Sequence 852952,	
c	22	14.8	74.0	25	13	US-11-036-317-724665	
c	23	14.8	43	9	US-10-783-557-428	Sequence 428_APP	
c	24	14.4	72.0	19	14	US-11-033-784-369550	Sequence 369550,
c	25	14.4	72.0	19	14	US-11-033-784-124405	Sequence 124405,
c	26	14.4	72.0	19	15	US-11-111-244-124405	Sequence 124405,
c	27	14.4	72.0	19	15	US-10-719-956-583062	Sequence 583062,
c	28	14.4	72.0	25	8	US-10-719-956-604657	Sequence 604657,
c	29	14.4	72.0	25	9	US-10-719-900-7136	Sequence 7136_AP
c	30	14.4	72.0	25	9	US-10-719-900-299394	Sequence 299394,
c	31	14.4	72.0	25	9	US-10-719-900-589698	Sequence 589698,
c	32	14.4	72.0	25	13	US-11-036-317-15619	Sequence 15619,
c	33	14.4	72.0	25	13	US-11-036-317-228611	Sequence 228611,
c	34	14.4	72.0	25	13	US-11-036-317-238611	Sequence 238611,
c	35	14.4	72.0	25	13	US-11-036-317-26809	Sequence 26809,
c	36	14.4	72.0	25	13	US-11-036-317-31495	Sequence 31495,
c	37	14.4	72.0	25	13	US-11-036-317-359559	Sequence 359559,
c	38	14.4	72.0	25	13	US-11-036-317-58660	Sequence 58660,
c	39	14.4	72.0	25	13	US-11-036-756-134735	Sequence 134735,
c	40	14.4	72.0	25	13	US-11-121-841-412943	Sequence 412943,
c	41	14.2	71.0	21	10	US-10-817-918-6600	Sequence 6600,
c	42	14.2	71.0	21	11	US-10-310-914A-28845	Sequence 28845,
c	43	14.2	71.0	25	6	US-10-322-438-17	Sequence 17_APPL
c	44	14.2	71.0	25	6	US-10-137-765-32	Sequence 32_APPL

GENERAL INFORMATION

RESULT 1
 US-10-766-185-1/c
 Publication No. US20040152655A1

APPLICANT: Yoon, Heejong
 Lee, Young Bok
 APPLICANT: Mao, Lingjun
 APPLICANT: Jiang, Xiaoming

TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
 FILE REFERENCE: REX 7034

CURRENT APPLICATION NUMBER: US/10/766, 185
 CURRENT FILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 130
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: human

US-10-766-185-1

Query Match Similarity 100.0%; Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4-2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATGGCCACCAGTGTCCAA 20
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 DQ 20 AATGAGCCACCAGTGTCCAA 1

RESULT 2
 US-10-766-185-2
 Sequence 517759,
 Sequence 289663,
 Sequence 41993,
 Sequence 852952,
 Sequence 7136_APPL
 Sequence 369550,
 Sequence 124405,
 Sequence 124405,
 Sequence 583062,
 Sequence 604657,
 Sequence 7136_APPL
 Sequence 299394,
 Sequence 589698,
 Sequence 15619,
 Sequence 228611,
 Sequence 238611,
 Sequence 26809,
 Sequence 31495,
 Sequence 359559,
 Sequence 58660,
 Sequence 134735,
 Sequence 412943,
 Sequence 6600,
 Sequence 28845,
 Sequence 17_APPL
 Sequence 32_APPL

APPLICANT: Yoon, Heejong
 APPLICANT: Lee, Chang Ho
 APPLICANT: Lee, Young Bok
 APPLICANT: Mao, Lingjun

Publication No. US20040152655A1
 GENERAL INFORMATION:
 APPLICANT: Yoon, Heejong
 APPLICANT: Lee, Chang Ho
 APPLICANT: Lee, Young Bok

```

; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; PRIORITY NUMBER: US 10/304,126
; PRIORITY FILING DATE: 2002-11-23
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE: antisense oligonucleotide
; OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-2

Query Match          100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;2; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy      1 ATATGAGGCCACCACTGTCCAA 20
Db      1 ATATGAGGCCACCACTGTCCAA 20

RESULT 3
US-10-190-394-2
Sequence 2, Application US/10190394
Publication No. US20030018007A1
GENERAL INFORMATION:
APPLICANT: Vincent, Karen
APPLICANT: Gregory, Richard
APPLICANT: Vincent, Karen
TITLE OF INVENTION: Compositions and Methods for Inducing Gene
FILE REFERENCE: GA0112CIP2
CURRENT APPLICATION NUMBER: US/10/190,394
CURRENT FILING DATE: 2002-07-03
PRIORITY APPLICATION NUMBER: US/09/579,897
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/1067,546
PRIORITY FILING DATE: 1997-12-04
PRIORITY APPLICATION NUMBER: PCT/US98/25753
PRIORITY FILING DATE: 1998-12-04
PRIORITY APPLICATION NUMBER: 09/133,612
PRIORITY FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 37
TYPE: DNA
ORGANISM: Homo sapiens
US-10-190-394-2

Query Match          92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29; Mismatches 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy      1 ATATGAGGCCACCACTGTCCAA 20
Db      8 ATATGAGGCCACCACTGTCCAA 27

RESULT 4
US-10-719-370A-187
Sequence 2, Application US/10719370A
Publication No. US20040220393A1
GENERAL INFORMATION:
APPLICANT: Ward, Donna T.
APPLICANT: Bobbie, Kenneth W.
APPLICANT: Marcusson, Eric G.
APPLICANT: Freier, Susan M.
TITLE OF INVENTION: MODULATION OF HIF1 $\alpha$  AND HIF2 $\alpha$  EXPRESSION
FILE REFERENCE: ISPM-1010
CURRENT APPLICATION NUMBER: US/10/719,370A

Query Match          100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;2; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy      1 ATATGAGGCCACCACTGTCCAA 20
Db      1 ATATGAGGCCACCACTGTCCAA 20

RESULT 5
US-11-083-794-225584/C
Sequence 225584, Application US/11083784
Publication No. US2005024547A1
GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Khorrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIORITY APPLICATION NUMBER: US/10/714,333
PRIORITY FILING DATE: 2003-11-14
PRIORITY APPLICATION NUMBER: 60/502,050
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIORITY FILING DATE: 2002-11-14
PRIORITY APPLICATION NUMBER: 60/426,137
PRIORITY FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 225584
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-794-225584

Query Match          82.0%; Score 16.4; DB 14; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy      1 ATATGAGGCCACCACTGTCC 18
Db      18 ATATGAGGCCACCACTGTCC 1

RESULT 6
US-11-101-244-225584/C
Sequence 225584, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Khorrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

```

CURRENT APPLICATION NUMBER: US11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIORITY APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIORITY APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 225584
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-225584

Query Match Best Local Similarity 82.0%; Score 16.4; DB 15; Length 19;
; Matches 17; Conservative 94.4%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
; Qy 1 ATGAGGCCACAGTGTC 19
; Db .18 AGTGAGCCACCACTGTGTC 1

RESULT 7
; US-10-310-91A-195175
; Sequence 15175, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bintwich, Isaac
; APPLICANT: Shlifer, Krutz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US10/310,91A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1398402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 195175
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
; US-10-310-91A-195175

Query Match Best Local Similarity 80.0%; Score 16; DB 11; Length 24;
; Matches 14; Conservative 87.5%; Pred. No. 5e+02; Indels 0; Gaps 0;
; Qy 5 AGCCACCACTGTGTC 20
; Db 1 AGCCACCACTGTGTC 16

RESULT 8
; US-10-719-900-515021/c
; Sequence 515021, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIORITY APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 515021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-515021

Query Match Best Local Similarity 77.0%; Score 15.4; DB 8; Length 25;
; Matches 16; Conservative 94.1%; Pred. No. 1e+03; Indels 0; Gaps 0;
; Qy 1 AATGAGGCCACAGTGTC 17
; Db 17 AATGAGGCCACAGTGTC 1

RESULT 9
; US-11-121-849-650902/c
; Sequence 650902, Application US/11121849
; Publication No. US20050277080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIORITY APPLICATION NUMBER: US11/121,949
; PRIORITY APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 650902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-650902

Query Match Best Local Similarity 89.5%; Score 15.8; DB 15; Length 25;
; Matches 17; Conservative 89.5%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
; Qy 1 ATATGGCCACAGTGTC 19
; Db 21 ATTGAGCCACAGTGTC 3

RESULT 10
; US-10-719-956-334675/c
; Sequence 334675, Application US/10719956
; Publication No. US2004016910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIORITY APPLICATION NUMBER: 60/427,836
; PRIORITY FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 334675
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-334675

Query Match Best Local Similarity 77.0%; Score 15.4; DB 8; Length 25;
; Matches 16; Conservative 94.1%; Pred. No. 1e+03; Indels 0; Gaps 0;
; Qy 1 AATGAGGCCACAGTGTC 17
; Db 17 AATGAGGCCACAGTGTC 1

RESULT 11
; US-10-719-900-571979/c
; Sequence 571979, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35281.
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 983914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 571979
LENGTH: 25

TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-571979

RESULT 12

Query Match 77.0%; Score 15.4; DB 9; Length 25;
Best Local Similarity 94.1%; Pred. No. 1e+03; 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAGGCCACCAAGTGCCA 19
Db 19 TGACCCACCAAGTGCCA 3

US-11-121-849-650903/C
Sequence 650903, Application US/11121849
Publication No. US2005022080A1

GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIORITY APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 650903
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-650903

Query Match 77.0%; Score 15.4; DB 15; Length 25;
Best Local Similarity 94.1%; Pred. No. 1e+03; 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGGCCACACTGTC 17
Db 18 ATGAGGCCACACTGAC 2

RESULT 13

US-11-121-849-650975
Sequence 650975, Application US/11121849
Publication No. US2005022080A1

GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIORITY APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 650975
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-650975

RESULT 14

Query Match 76.0%; Score 15.2; DB 15; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.3e+03; 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGCCA 20
Db 1 AATGAGCCACCAAGTGCCA 20

US-11-083-794-1242371
Sequence 1242371, Application US/11083784
Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khorrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1242371
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-794-1242371

RESULT 15

US-11-101-244-1242371
Sequence 1242371, Application US/11101244
Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khorrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1242371
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-121-849-650975

US-11-101-244-1242371

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Query Match          74.0%; Score 14.8; DB 15; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.1e-03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0
Qy   2 ATGAGCCACCACTGGTCCA 19
      :|||||:|||||:|||:
Db   2 AUGAGCCACCAUAGUCUA 19

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Search completed: May 21, 2006, 22:32:02
Job time : 656 secs

Run on: May 21, 2006, 22:18:38 ; Search time 32.5 Seconds
 copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using bw model

Title:	US-10-766-185-2
Perfect score:	20
Sequence:	1. atggaggccaccagtgtccaa 20
Scoring table:	IDENTITY_NUC
Gappen:	10.0 , Gapext 1.0
Searched:	224314 seqs, 35277956 residues
Total number of hits satisfying chosen parameters:	38744
Minimum DB seq length:	0
Maximum DB seq length:	50

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Result No.	Score	Query Match Length	DB ID	Description
C 1	14.2	71.0	25	US-11-217-529-13735
C 2	13.2	66.0	25	US-11-217-529-44186
C 3	13.2	66.0	25	US-11-217-529-44186
C 4	13.2	66.0	25	US-11-217-529-44186
C 5	13	65.0	50	US-10-511-937-2733
C 6	13	65.0	25	US-11-217-529-74193
C 7	12.8	64.0	25	US-11-217-529-88752
C 8	12.8	64.0	25	US-11-217-529-9148
C 9	12.6	63.0	25	US-11-217-529-17069
C 10	12.6	63.0	25	US-11-217-529-22469
C 11	12.6	63.0	25	US-11-217-529-22526
C 12	12.4	62.0	25	US-11-217-529-8089
C 13	12.4	62.0	25	US-11-217-529-45366
C 14	12.2	61.0	25	US-11-217-529-22471
C 15	12.2	61.0	25	US-11-217-529-38860
C 16	12.2	61.0	25	US-11-217-529-4089
C 17	12.2	61.0	25	US-11-217-529-89698
C 18	12.2	61.0	25	US-11-217-529-110177
C 19	12.2	61.0	25	US-11-217-529-132345
C 20	12.2	61.0	25	US-11-217-529-159967
C 21	12.2	61.0	26	US-11-217-502-110
C 22	12	60.0	25	US-11-217-529-30855
C 23	12	60.0	25	US-11-217-529-33629
C 24	12	60.0	25	US-11-217-529-3480
C 25	12	60.0	25	US-11-217-529-56109

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	LENGTH:	TYPE:	SEQUENCE
1	25	DNA	ATGGAGGCCACCAGTGTCCAA
2	13735	DNA	ATGGAGGCCACCAGTGTCCAA
3	44186	DNA	ATGGAGGCCACCAGTGTCCAA
4	2733	DNA	ATGGAGGCCACCAGTGTCCAA
5	74193	DNA	ATGGAGGCCACCAGTGTCCAA
6	88752	DNA	ATGGAGGCCACCAGTGTCCAA
7	17069	DNA	ATGGAGGCCACCAGTGTCCAA
8	22469	DNA	ATGGAGGCCACCAGTGTCCAA
9	22526	DNA	ATGGAGGCCACCAGTGTCCAA
10	8089	DNA	ATGGAGGCCACCAGTGTCCAA
11	132345	DNA	ATGGAGGCCACCAGTGTCCAA
12	159967	DNA	ATGGAGGCCACCAGTGTCCAA
13	110177	DNA	ATGGAGGCCACCAGTGTCCAA
14	22471	DNA	ATGGAGGCCACCAGTGTCCAA
15	38860	DNA	ATGGAGGCCACCAGTGTCCAA
16	4089	DNA	ATGGAGGCCACCAGTGTCCAA
17	89698	DNA	ATGGAGGCCACCAGTGTCCAA
18	110175	DNA	ATGGAGGCCACCAGTGTCCAA
19	132345	DNA	ATGGAGGCCACCAGTGTCCAA
20	159967	DNA	ATGGAGGCCACCAGTGTCCAA
21	22471	DNA	ATGGAGGCCACCAGTGTCCAA
22	30855	DNA	ATGGAGGCCACCAGTGTCCAA
23	33629	DNA	ATGGAGGCCACCAGTGTCCAA
24	3480	DNA	ATGGAGGCCACCAGTGTCCAA
25	56109	DNA	ATGGAGGCCACCAGTGTCCAA

RESULT 1

US-11-217-529-13735/c

; Sequence 13735, Application US/11217529
 Publication No. US200600099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAMURA, NORIMASA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT ILLING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-03-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: Patentin version 3.3

; SEQ ID NO: 13735

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

; US-11-217-529-13735

Query Match Score 71.0%; Score 14.2; DB 7; Length 25;
 Best Local Similarity 84.2%; Pred. No. 21;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGGAGGCCACCAGTGTCCAA	19
Db	24	ACTGAGGCCACCAGTGTCCAA	6

RESULT 2

US-11-217-529-44186/c

; Sequence 44186, Application US/11217529

; Publication No. US200600099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIIRO

; APPLICANT: NAKAMURA, NORIHIKO

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

```

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 44186
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-44186

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 71; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGAGGCCACCACTTCC 18
Db 22 ATGAGACCACGGCTTC 5

RESULT 3
US-11-217-529-86968
; Sequence 86968, Application US/11217529
; Publication No. US20060099612A1
GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY NUMBER: US 10/932,182
PRIORITY FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SBO ID NO: 86968
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-86968

Query Match 65.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 71; Mismatches 0; Indels 3; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ATGAGGCCACCACTTCC 19
Db 4 ATGAGGCCACCATTCCTA 21

RESULT 4
US-10-511-937-213/C
; Sequence 213, Application US/10511937
; Publication No. US2006008836A1
GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: FRTY, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LY, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIORITY APPLICATION NUMBER: PCT/US2003/012946

Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 82; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TAGGCCACCACTTCCAA 20
Db 22 TGAACACACAGTGACCAA 5

RESULT 5
US-11-217-529-74193/C
; Sequence 74193, Application US/11217529
; Publication No. US20060099612A1
GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY APPLICATION NUMBER: US 10/932,182
PRIORITY FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 74193
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-74193

Query Match 65.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ATGAGGCCACCACTTCC 14
Db 22 ATGAGGCCACCAT 10

RESULT 6
US-11-217-529-88752/C
; Sequence 88752, Application US/11217529
; Publication No. US20060099612A1
GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY APPLICATION NUMBER: US 10/932,182
PRIORITY FILING DATE: 2004-09-02

```

NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88752
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*
; US-11-217-529-88752

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Gaps 0;

Qy 1 ATGAGGCCACCAAG 13
Db 18 ATGAGGCCACCAAG 6

RESULT 7
US-11-217-529-9748
Sequence 9748, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIWA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY NUMBER: US 10/932,182
PRIORITY FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9748
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
US-11-217-529-9748

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Gaps 0;

Qy 4 GAGGCCACCAAGTCCA 19
Db 7 GAGGCCATCAGGGTCCA 22

RESULT 8
US-11-217-529-117069
Publication No. US20060099612A1
SEQUENCE INFORMATION:
Sequence 117069, Application US/11217529
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIWA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 117069
LENGTH: 25
TYPE: DNA

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 2 ATGAGGCCACCAAGTCCA 20
Db 4 AAGAGGCCACCTTGCCAA 22

RESULT 10
US-11-217-529-7164/c
Sequence 71644, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIWA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIORITY FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 71644
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
US-11-217-529-71644

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 19
Db 24 AAAGAGCCACCAAGGTGTACA 6

RESULT 11

; Sequence 125526, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-125526

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAGCCACCAAGTGTCCA 19
Db 1 ATGACCCAGCTGTGACCA 19

RESULT 12

; Sequence 8089, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-8089/c

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAGCCACCAAGTGTCCA 19
Db 1 ATGACCCAGCTGTGACCA 19

RESULT 13

; Sequence 45366, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-45366

Query Match 62.0%; Score 12.4; DB 7; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.9e+02; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCACCAAGTGTCCA 20
Db 7 CCACCAAGTGTCCA 20

RESULT 14

; Sequence 29471, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-29471

Query Match 61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.4e+02; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAGCCACCAAGTGTCCA 20
Db 21 GAGCCACCATCTCCAA 5

RESULT 15

; Sequence 38860, Application US/11217529

US-11-217-529-38860/c

Query Match 62.0%; Score 12.4; DB 7; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.9e+02; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGCCACCAAGTGTCCA 17
Db 18 GAGCCACTAGTGTCCA 5

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-3B-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-03-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 38860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-38860

Query Match 61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Prcd. No. 2.4e-02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GAGCCACCACTGTCCA 20
DB 21 GAGTACACGAGTGACA 5

Search completed: May 21, 2006, 22:34:13
Job time : 32.5 secs

Commercially supplied Qiagen HotStar buffer

184 פָּתַח יְהוּדָה וְשָׁמֶן: 0:23 מִתְבֵּן (וְיָרַגְנֵן) מִכְּלָנָה /

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

FEATURES

source

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organism="SUS Scrofa"
/mol_type="genomic DNA"
/strains="white composite"
/fengjing="crossover"
/db_xref="taxon:9823"
/sex="male and female"
/clone.lib="SCP - porc"
/dev_stages="adult"
/note=Organ: spleen"
<1. .>92
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SIS

Qy	Best Local 20; Conservative 0;	Score 100.0%;	DB 7;	Length 492;
Db	Matches 0;	Pred. No. 2.8e+02;	Mismatches 0;	Indels 0;
	1 ATGAGGCCACCTGTGCCAA	20	75	0;
RESULT 2				
G72558/c				
DEFINITION	MARC 6633-6632:99007336:1 SCP - porcine spleen	928 bp	DNA	linear
LOCUS	GT2558			Sub scrofa STS
ACCESSION	GT2558			genomic, sequence tagged site.
VERSION	GT2558.1			
KEYWORDS	STS.			
SOURCE	Sub scrofa (pig)			
ORGANISM	Sub scrofa			
MATERIAL	Maekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Sub-	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;			
REFERENCE	Kele, J.W., Fahrnburg, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L. and			
AUTHORS	1 (bases 1 to 928)			
TITLE	Fahrnburg, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L. and			
JOURNAL	Single nucleotide polymorphism (SNP) discovery in expressed porcine			
COMMENT	genes			
	Unpublished (2001)			
Contact:	Freking BA			
USDA, ARS, US Meat Animal Research Center				
PO Box 166, Clay Center, NE 68933-0166, USA				
Tel: 402 762 4278				
Fax: 402 752 4173				
Email: freking@email.marc.usda.gov				
Primer A: TGTGAACTTAATGCTCTATA				
Primer B: AAAAGGAGTGTATAGGCAC				
STS Bize: 560				
PCR Profile:				
Hotstart:	95 degrees for 15 minutes			
Denature:	95 degrees for 30 seconds			
Anneal:	55 degrees			
Extension:	68 degrees for 2 minutes			
Cycles:	32 to 45			
Protocol:				
Template:	50-200 ng genomic DNA			
Primer:	each 20 pmoles			
dNTPs:	each 88 uM			

STS /notes="Urgah: spleen."
<1. .>928

1

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Query Match          100.0%; Score 20; DB 67; Length 492;
Best Local Similarity      100.0%; Pred. No. 2. 8e-02; Mismatches 0;
Matches 20; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
Qy
  1 AATGACCCACCAAGTGTCAA 20
  ||||| | | | | | | | | | |
  94 AATGACCCACCAAGTGTCAA 75

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G72558/c
16mm

372558/G
222222

DEFINITION
Locus G42558
MARC 6633-6692:992007336:1 SCP - porcine spleen linear SIS U+**AUG-2001**
ACCESSION G72558
VERSION G72558.1
KEYWORDS genomic, sequence tagged site.
SOURCE STS.
ORGANISM *Sus scrofa* (pig)

ORGANISM Sub scrota Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Monotremata; Diplopoda; Insecta; Diptera; Culicidae; Culex quinquefasciatus

REFERENCE 1 (pages 1 to 928)
Sub. *Mammalia; Butterilia; Mammals; Butterflies; Cetartiodactyla; Suina; Suidae;*

AUTHORS Fahrnkug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L. and Keef, T.W.

TITLE Single nucleotide polymorphism (SNP) discovery in expressed porcine genes

JOURNAL COMMENT Unpublished (2001)

Contact: Preking BA
USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278

Pax: 402 762 4173
Email: freking@email.marc.usda.gov

Primer A: TGTGAACTTAATCTCCATA
Primer B: AAAAGGATGTTATAGGGAC
GTS Size: 560
PCR Profile:

Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds

Anneal: 58 degrees
Extension: 68 degrees for 2 minutes

Protocol: Cycles: 32 to 45

Template: 50-200 ng genomic DNA
primer: each 20 pmoles
dNTPs: each 88 uM

ORIGIN /clone-lib="lambda ZAP I I cDNA"
PolyA_signal 1229..1234

Db 2549 AATGAGCCACAGTGTCCA 2530
RESULT 4

Query Match 100.0%; Score 20; DB 5; Length 1252;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATGAGCCACAGTGTCCA 20
Db 126 AATGAGCCACAGTGTCCA 107

RESULT 5
Db DQ229099/C
LOCUS DQ229099 mRNA linear ROD 29-OCT-2005
DEFINITION Bospalax baileyi hypoxia inducible factor 1 alpha subunit mRNA, complete cds.
ACCESSION DQ229099
VERSION DQ229099.1 GI:78058355
KEYWORDS:

SOURCE Bospalax baileyi
ORGANISM Bospalax baileyi
Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Sciurognathi; Muridae; Spalacidae; Myospatracinae; Bospalax.
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
TITLE Cloning of hypoxia-inducible factor 1 alpha from plateau zokor (Myospatrax baileyi).
JOURNAL Unpublished

REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE Submitted (22-MAR-2005) Department of Biotechnology, College of Life Sciences, Room 229, Teaching Building Bright, Yuzhan Campus, Hangzhou, Zhejiang 310027, PR China
AUTHORS Location/Qualifiers

FEATURES source
JOURNAL Direct submission
REFERENCE 2. (bases 1 to 3013)
AUTHORS Xie, Z.-Y., Chen, X.-Q., Du, J.-Z., Li, H.-Q., Wang, T.-Y. and Xiao, P.-H.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2005) Department of Biotechnology, College of Life Sciences, Room 229, Teaching Building Bright, Yuzhan Campus, Hangzhou, Zhejiang 310027, PR China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

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AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

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REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
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REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

FEATURES source
JOURNAL Direct submission
REFERENCE 1. (bases 1 to 3217)
AUTHORS Chen, X.-Q., Xie, Z.-Y. and Du, J.-Z.
JOURNAL Submitted (03-OCT-2005) Division of Neurobiology and Physiology, Zhejiang University, Zheha Road 38#, Teaching Building 8, Room 229, Yuquan Campus, Hangzhou, Zhejiang 310027, China

RESULT 6
Db AY621118/C
LOCUS AY621118 mRNA linear MAM 07-JUN-2004
DEFINITION Bos grunniens hypoxia inducible factor-1a (HIF-1a) mRNA, complete cds.
ACCESSION AY621118
VERSION AY621118.1 GI:47933908

KEYWORDS	Bos grunniens (domestic yak)
SOURCE	Bos grunniens
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bivalvia; Bovinae; Bos.
REFERENCE	1 (bases 1 to 3296)
AUTHORS	Dolt, K.S. and Qadar Pasha, M.A.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAY-2004) Functional Genomics Unit, Institute of Genomics and Integrative Biology, Mall Road, Delhi 110007, India
FEATURES	Location/Qualifiers
Source	1. .>296 /organism="Bos grunniens" /mol_type="mRNA" /db_xref="taxon:30521"
CDS	1. .>296 /gene="HIF-1A" 2. .2473 /gene="HIF-1A" /note="BH4 transcription factor" /codon_start=1 /product="hypoxia inducible factor-1a" /protein_id="ATM39520.1" /db_xref="GI:4933909" /translation="MEGAGANDRKKISSRRKEKSRDAARSRRSKESERVYELAHOLPUPHVSILDKASVWVNGKLTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE LTDGDMIVTSVNVKNGLQTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE ONTOFSFLRKKCTTSRGTMNTISATVTKLHTCHIYHDTNSNQSCGGYKCPMT CLVLCRIPHNSRIPPLSKTSRHSUDMKSSCDRTELMGYPEBLGRSY BYHALDSHILTKHDMFKQVTTGQTMILAKGGYVWETQVINTKNSQPC IVCVNVVVGIGTQHDLIFSIQQTETVLPKPSDDNMKLOPLTKTSESDLSFLKLK SPDDATLLAPAGGTTISLQRGNTTDDQLEPLVPLVLYDUMVLSNEKLONILAM SPUPSETPKLSKADPAQNLQEVALKLNPNESALSFMPQQQDAPSDESTRO SSPPENSPSBZCFDPDSWNBPKLVEVKLPAFTEAKNPSPDFTDIDEMAPYI TDGKEDIKLIAFFSPHPKPEPCATSPYSDGSRTASPNNRKGKGTIEQERKSH RSPNVLVAQSRTTAPERSLNPKLALQWQRKTRKTDGSLQFQAVGVLTLQQPDB RATTSLSWKRYKQSSBONGMECKTILIPSDACRILQGQMSDGLPQLQSYDCB VNAPIQSGRNLUQGELLRLAQDN" 2474..>3296 /gene="HIF-1A"
ORIGIN	3' UTR
Query Match	100.0%; Score 20; DB 14; Length 3296;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;
Matches	20; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
Qy	1 ATGACCACCGTGTCAA 20
Db	2519 ATGACCCACCGTGTCAA 2500
RESULT	7
DEFINITION	Macaca fascicularis testis cDNA, clone: Qtsa-19088, similar to human hypoxia-inducible factor 1, alpha subunit (basichelix-loop-helix transcription factor) (HIF1A), transcript variant 1, mRNA, RefSeq: NM_001530.2.
ACCESSION	AB169332
VERSION	AB169332.1
KEYWORDS	oigo capping; fib (full insert sequence).
SOURCE	Macaca fascicularis (crab-eating macaque)
ORGANISM	Macaca fascicularis
REFERENCE	Mammalia; Eutheria; Burchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
AUTHORS	Osada, N., Hirata, M., Tamura, J., Hida, M., Suzuki, Y., Sugano, S., Gotohori, T., Shen, C.-K.J., Wu, C.-I. and Hashimoto, K.
TITLE	Substitution and Structural Divergence of 5'-UTR Evolution: Comparative Analysis Between Human and Cynomolgus Monkey cDNAs
FEATURES	Location/Qualifiers
Source	1. .3669 /organism="Macaca fascicularis" /mol_type="mRNA" /db_xref="taxon:9541" /clones="Qtsa-19088" /sex="mal" /clone_libr="macaque cDNA library Qtsa" /dev_stage="adult" 2.7..2777 /note="unnamed protein product; Homo sapiens hypoxia-inducible factor 1, alpha subunit (basichelix-loop-helix transcription factor) (HIF1A), transcript variant 1, mRNA, RefSeq: NM_001530.2" /codon_start=1 /protein_id="BAB01417.1" /db_xref="GI:6791046" /translation="MEGAGANDRKKISSRRKEKSRDAARSRRSKESERVYELAHOLPUPHVSILDKASVWVNGKLTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE LTDGDMIVTSVNVKNGLQTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE ONTOFSFLRKKCTTSRGTMNTISATVTKLHTCHIYHDTNSNQSCGGYKCPMT CLVLCRIPHNSRIPPLSKTSRHSUDMKSSCDRTELMGYPEBLGRSY BYHALDSHILTKHDMFKQVTTGQTMILAKGGYVWETQVINTKNSQPC IVCVNVVVGIGTQHDLIFSIQQTETVLPKPSDDNMKLOPLTKTSESDLSFLKLK SPDDATLLAPAGGTTISLQRGNTTDDQLEPLVPLVLYDUMVLSNEKLONILAM SPUPSETPKLSKADPAQNLQEVALKLNPNESALSFMPQQQDAPSDESTRO SSPPENSPSBZCFDPDSWNBPKLVEVKLPAFTEAKNPSPDFTDIDEMAPYI TDGKEDIKLIAFFSPHPKPEPCATSPYSDGSRTASPNNRKGKGTIEQERKSH RSPNVLVAQSRTTAPERSLNPKLALQWQRKTRKTDGSLQFQAVGVLTLQQPDB RATTSLSWKRYKQSSBONGMECKTILIPSDACRILQGQMSDGLPQLQSYDCB VNAPIQSGRNLUQGELLRLAQDN" 2474..>3296 /gene="HIF-1A"
COMMENT	The International consortium for macaque cDNA sequencing and analysis consists of: Department of Virology and Human Genome, Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; Division of Genetic Resources, National Institute of Infectious Diseases of Japan, Tokyo, Japan; National Health Research Institute, Taipei, Taiwan; Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; Center for Information Biology, National Institute of Genetics of Japan, Mishima, Japan; http://www.nih.go.jp/yoken/genbank/ Lab host: TOPO Vector: PME18S-FL3 (Acc.no. AB009864) Site: Draft (GACTCTGTG) R. Site2: Draft (CACCATCTG)
Description	1st strand cDNA was primed with an oligo(dT) primer (ATGGCCTTCTTCTTCTTCTT), double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments < 1.5kb. The SfiI-digested PCR product was cloned into distinct Draft sites or pME18S-FL3. XbaI sites just outside the Draft sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Libraries were made from: Occe: cerebellum cortex Otpa: parietal lobe Ota: temporal lobe right Ofla: frontal lobe left Omoa: medulla oblongata Obsa: brain stem Oora: occipital lobe right Qtsa: testis Custom primers were used for 5' and 3'-end sequencing. The full-insert sequencing was done by primer-walking method using ABI DNA sequencer. Location/Qualifiers
FEATURES	Source
CDS	1. .3669 /organism="Macaca fascicularis" /mol_type="mRNA" /db_xref="taxon:9541" /clones="Qtsa-19088" /sex="mal" /clone_libr="macaque cDNA library Qtsa" /dev_stage="adult" 2.7..2777 /note="unnamed protein product; Homo sapiens hypoxia-inducible factor 1, alpha subunit (basichelix-loop-helix transcription factor) (HIF1A), transcript variant 1, mRNA, RefSeq: NM_001530.2" /codon_start=1 /protein_id="BAB01417.1" /db_xref="GI:6791046" /translation="MEGAGANDRKKISSRRKEKSRDAARSRRSKESERVYELAHOLPUPHVSILDKASVWVNGKLTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE LTDGDMIVTSVNVKNGLQTQFELTGHASVDFDFTPCDHREMELTHRLNGLVKGKE ONTOFSFLRKKCTTSRGTMNTISATVTKLHTCHIYHDTNSNQSCGGYKCPMT CLVLCRIPHNSRIPPLSKTSRHSUDMKSSCDRTELMGYPEBLGRSY BYHALDSHILTKHDMFKQVTTGQTMILAKGGYVWETQVINTKNSQPC IVCVNVVVGIGTQHDLIFSIQQTETVLPKPSDDNMKLOPLTKTSESDLSFLKLK SPDDATLLAPAGGTTISLQRGNTTDDQLEPLVPLVLYDUMVLSNEKLONILAM SPUPSETPKLSKADPAQNLQEVALKLNPNESALSFMPQQQDAPSDESTRO SSPPENSPSBZCFDPDSWNBPKLVEVKLPAFTEAKNPSPDFTDIDEMAPYI TDGKEDIKLIAFFSPHPKPEPCATSPYSDGSRTASPNNRKGKGTIEQERKSH RSPNVLVAQSRTTAPERSLNPKLALQWQRKTRKTDGSLQFQAVGVLTLQQPDB RATTSLSWKRYKQSSBONGMECKTILIPSDACRILQGQMSDGLPQLQSYDCB VNAPIQSGRNLUQGELLRLAQDN" 2474..>3296 /gene="HIF-1A"

Harvey, Y., Havlik, S., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogies, M., Hollins, B., Howell, S., Hulyk, S., Hume, J., Idlesbord, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Kelly-S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levant, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenzana, L., Lousegé, H., Lozado, R.J., Lu, X., Ma, J., Malenová, M., Mahindaratne, M., Mahmoud, M., Mailly, K., Mangum, A., Mangum, B., Mapus, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milova, V., Milovac-Jevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.edu/doc/Genbank-draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 19 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

JOURNAL	Submitted (25-JAN-2005) Human Genome Sequencing Consortium	Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 248982)	
AUTHORS	Cow Genome Sequencing Consortium.	
TITLE	Direct Submission	
COMMENT	Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
On Jun 28, 2005 this sequence version replaced gi:5802190.		
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.		
-----	Genome Center	FEATURES
Center code: BCM		source
Web site: http://www.hgsc.bcm.tmc.edu/		
Contact: hgsc-help@bcm.tmc.edu		
-----	Project Information	
Center project name: PCOV		
Center clone name: CH240-47113		
-----	Summary Statistics	
Assembly program: Atlas 3.0;	gap	
Consensus quality: 241678 bases at least Q40	gap	
Consensus quality: 243820 bases at least Q30	gap	
Consensus quality: 245399 bases at least Q20	gap	
Estimated insert size: 246581; sum-of-contigs estimation	gap	

23590	236089: gap of unknown length	
236090	242226: contig of 6137 bp in length	
	242227: gap of 50 bp	
	242227: 244358: contig of 2082 bp in length	
	244359: 244458: gap of unknown length	
	244459: 245460: contig of 1002 bp in length	
	245461: 245560: gap of unknown length	
	245561: 246564: contig of 1004 bp in length	
	246565: 246664: gap of unknown length	
	246665: 247679: contig of 1015 bp in length	
	247680: 247779: gap of unknown length	
	247780: 248982: contig of 1203 bp in length	
	Location/Qualifiers	
	1. .44982	
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	/mol_type="genomic DNA"	
	/db_xref="taxon:9913"	
	/clone="CH240-47113"	
	75230. .75279	
	/estimated.length=50	
	88089. .88731	
	/estimated.length=643	
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	/estimated.length=50	
	12110. .121159	
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	122705. .122754	
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	142001. .142050	
	/estimated.length=50	
	154656. .154715	
	/estimated.length=50	
	157021. .157070	
	/estimated.length=50	
	160057. .160116	
	/estimated.length=50	

gap 164002..164051
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 gap 226342..226391
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 gap 230590..230639
 /estimated_length=50
 235930..235989
 /estimated_length=unknown
 242227..242276
 /estimated_length=50
 gap 244359..244458
 /estimated_length=unknown
 245461..245560
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 246565..246664
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 247680..247779
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Query Match 100.0%; Score 20; DB 12; Length 248982;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCACTGTCCA 20
 Db 187060 ATGGAGCCACCACTGTCCA 187079

RESULT 10

AX986444/c
 DEFINITION AX986444 311 bp DNA linear PAT 15-JAN-2004
 LOCUS Sequence 17247 from Patent EP104808.
 ACCESSION AX986444
 VERSION AX986444.1 GI:40992584
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
 AUTHORS ESTs and encoded human proteins
 TITLE Patent: EP 1104808-A 17247 06-JUN-2001;
 JOURNAL Genet (FR)

FEATURES Source
 . Location/Qualifiers
 1. .311
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 311;
 Best Local Similarity 95.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCACTGTCCA 20
 Db 198 ATGGAGCCACCACTGTCCA 179

RESULT 12

AR425750/c
 DEFINITION AR425750 311 bp DNA linear PAT 18-DEC-2003
 LOCUS Sequence 17247 from patent US 6639063.
 ACCESSION AR425750
 VERSION AR425750.1 GI:40180860
 KEYWORDS SOURCE Unknown.
 ORGANISM Unclassified.
 1. (bases 1 to 311)
 Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
 ESTs and encoded human proteins
 JOURNAL Patent: US 6639063-A 17247 28-OCT-2003;
 Genet S.A.;
 WOX;
 FEATURES Source
 . Location/Qualifiers
 1. .311
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 /mol_type="genomic DNA"

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 311;
 Best Local Similarity 95.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCACTGTCCA 20
 Db 198 ATGGAGCCACCACTGTCCA 179

RESULT 11

BD121303/c
 DEFINITION BD121303 311 bp DNA linear PAT 18-SEP-2002
 LOCUS EST and encoded human protein.
 ACCESSION BD121303
 VERSION BD121303.1 GI:23216213
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Query Match 92.0%; Score 18.4; DB 2; Length 311;
 Best Local Similarity 95.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCACTGTCCA 20
 Db 198 ATGGAGCCACCACTGTCCA 179

RESULT 13

CQ696751/c
 DEFINITION CQ696751 375 bp DNA linear PAT 03-FEB-2004
 LOCUS Sequence 41677 from Patent WO20070737.
 ACCESSION CQ696751

VERSION C0696751.1 GI:42246561
 KEYWORDS KCl: 50 mM
 SOURCE Tris-HCl: 10 mM
 PH: 9.3
 ORGANISM
 REFERENCE 1 Derived from abEST (genbank accession U22431).
 AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 41677 12-SEP-2002;
 Chondrogen Inc. (CA)
 FEATURES Location/Qualifiers
 SOURCE 1. .375
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match Best Local Similarity 92.0%; Score 18.4; DB 2; Length 375;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qv 1 AMTAGAGCCACCGATGTCCA 20
 Db 165 AGTGAGGCCACCGATGTCCA 146
 RESULT 14
 LOCUS G26793 1172 bp DNA linear STS 02-JUN-1996
 DEFINITION human STS STS_U22431, sequence tagged site.
 ACCESSION G26793
 VERSION G26793.1 GI:1349025
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bukay-Yoata, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 1172)
 AUTHORS Hudson,T.
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically
 Mapped STS
 JOURNAL Unpublished (1995)
 COMMENT Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900
 Fax: 617 252 1902
 Email: thudson@genome.wi.mit.edu
 Primer A: TGGACACTGGCTGCTCACTA
 Primer B: AAGCTACTGCATGCAATGG
 STS size: 223
 PCR Profile:
 Preboak:
 Denaturation: Annealing: 56 degrees C
 Polymerization: /db_xref="taxon:9606"
 PCR Cycles: 35
 Thermal Cycler:
 Protocol:
 Template: 10 ng
 Primer: each 5 pm
 dNTPs: each 4 nM
 Taq Polymerase: 0.025 units/uL
 Total Vol.: 20 uL
 Buffer:
 MgCl2: 1.5 mM

KCl: 50 mM
 Tris-HCl: 10 mM
 PH: 9.3

FEATURES source
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 /mol_type="genomic DNA"
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 31. .50
 ORIGIN
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 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 49 AGTGAGGCCACCGATGTCCA 30
 RESULT 15
 LOCUS HSIF1A13 1558 bp DNA linear PRI 26-OCT-1998
 DEFINITION Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene,
 exon 15 and complete cds.
 ACCESSION AF050127
 VERSION AF050127.1 GI:3790533
 KEYWORDS
 SEGMENT 13 of 13
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bukay-Yoata, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 1558)
 AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
 TITLE The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
 evolutionary conservation
 JOURNAL Genomics 52 (2), 159-165 (1998)
 REFERENCE 2 (bases 1 to 1558)
 AUTHORS Iyer,N.V., Leung,S.W. and Semenza,G.L.
 TITLE Direct Submission
 JOURNAL Submitted (24-FEB-1998) Departments of Pediatrics and Medicine,
 Institute of Genetic Medicine, Johns Hopkins University School of
 Medicine, 600 N. Wolfe St., Baltimore, MD 21287-3914, USA
 FEATURES Location/Qualifiers
 SOURCE 1. .1558
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="4"
 /map="1431-924"
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 AF050120.1:1..251,AF050121.1:1..422,AF050122.1:1..551,
 AF050123.1:1..527,AF050124.1:1..996,AF050125.1:1..551,
 /gene="HIF1A"
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 AF050121.1:134..281,AF050122.1:188..408,
 AF050123.1:120..406,AF050124.1:191..341,
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 AF050126.1:138..264,93..1413)
 /gene="HIF1A"
 /product="hypoxia-inducible factor 1 alpha subunit"

GenCore version 5.1.8										
Copyright (c) 1993 - 2006 Biocceleration Ltd.										
Om nucleic - nucleic search, using SW model										
Run on: May 21, 2006, 21:08:55 ; Search time 259.5 Seconds (Without alignments)										
537.360 Million cell updates/sec										
Title: US-10-766-185-2	c	19	18.4	92.0	3678	6	ABK84267			
Perfect score: 20	c	20	18.4	92.0	3678	8	ACB8893	Acb8893 Gene diff		
Sequence: 1 aatgagccaccagtgccaa 20	c	21	18.4	92.0	3678	10	AB203187	Ab203187 Toxicolog		
Scoring table: IDENTITY_NUC	c	22	18.4	92.0	3678	14	AED1794	Aed1794 Fibrotic		
Gapop 10.0 , Gapext 1.0	c	23	18.4	92.0	3736	2	ATT45937	Att45937 Human hyp		
Searched: 5244920 seqs, 348612431 residues	c	24	18.4	92.0	3736	3	AAZ89537	Aaz89537 DNA encod		
Total number of hits satisfying chosen parameters:	c	25	18.4	92.0	3736	9	ADU8530	Adu8530 Human DNA		
Minimum DB seq length: 0	c	26	18.4	92.0	3735	14	AEC09680	Aec09680 Human HIF		
Maximum DB seq length: 200000000	c	27	18.4	92.0	3812	12	ADG26976	Adg26976 Human HIF		
Post-processing: Minimum Match 0%	c	28	18.4	92.0	3927	6	AAS61690	Aas61690 Lung smal		
Maximum Match 100%	c	29	18.4	92.0	3933	2	AAK88980	Aak88980 Human tra		
Listing first 45 summaries	c	30	18.4	92.0	3933	8	ADA03184	Ad03184 Human Hif		
Database : N_GeneSeq8;*	c	31	18.4	92.0	3933	10	ADD18957	Add18957 Human dis		
1: geneseqn1990s;*	c	32	18.4	92.0	3933	11	ADP30301	Adp30301 Hypoxia-dis		
2: geneseqn2000s;*	c	33	18.4	92.0	3933	10	ADG89361	Adg89361 Cancer de		
3: geneseqn2001s;*	c	34	18.4	92.0	3933	10	ADG54154	Adg54154 Human PRO		
4: geneseqn2002s;*	c	35	18.4	92.0	3933	12	ADU8133	Adu8133 Human PRO		
5: geneseqn2003s;*	c	36	18.4	92.0	3933	12	ADV74936	Adv74936 DNA encod		
6: geneseqn2004s;*	c	37	18.4	92.0	3933	13	ADR24764	Adr24764 Breast ca		
7: geneseqn2005s;*	c	38	18.4	92.0	3933	13	ACN39703	Acn39703 Tumour-ab		
8: geneseqn2003bs;*	c	39	18.4	92.0	3933	13	ADP54154	Adp54154 Human PRO		
9: geneseqn2003bs;*	c	40	18.4	92.0	3933	13	ADT78563	Adt78563 Human HIF		
10: geneseqn2003bs;*	c	41	18.4	92.0	3933	13	ADT78434	Adt78434 Human HIF		
11: geneseqn2004as;*	c	42	18.4	92.0	3933	14	AUX97785	Aux97785 Human HYP		
12: geneseqn2004as;*	c	43	18.4	92.0	3958	12	ADQ26976	Adq26976 Human HIF		
13: geneseqn2005bs;*	c	44	18.4	92.0	3958	14	ADZ36287	Adz36287 Human HIF		
14: geneseqn2005bs;*	c	45	18.4	92.0	3958	14	ADZ67400	Adz67400 Different		
Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
Result No. Score Query Match Length DB ID Description	ALIGNMENTS									
1 20 100.0 20 13 ADQ88722	RESULT 1									
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c 20 100.0 27884 4 AAK7781	XX	AC ADQ88722;								
c 20 100.0 57500 13 ADT78441	XX	DT 21-OCT-2004 (first entry)								
c 20 100.0 57501 12 ADT7943	XX	DE Human HIF-1 antisense oligonucleotide RX-0047.								
c 18.4 92.0 37 2 AAX78996	XX	RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; BB; antisense oligonucleotide; antisense technology.								
c 18.4 92.0 1192 13 ADR1339	XX	KW								
c 18.4 92.0 2711 10 ADB25258	XX	OS Homo sapiens.								
c 18.4 92.0 3203 12 ADT16279	XX	PN US2004152655-A1.								
c 18.4 92.0 3229 9 ADA2406	XX	PD 05-AUG-2004.								
c 18.4 92.0 3229 10 ADP5615	XX	PR 28-JAN-2004; 2004US-00766185.								
c 18.4 92.0 3229 10 ADJ5307	XX	PR 31-JAN-2003; 2003US-0444367-P.								
c 18.4 92.0 3229 12 ADT6983	XX	PA (YOUN/) YOON H.								
c 18.4 92.0 3551 12 ADT4945	XX	PA (MAOL/) MAO L.								
c 18.4 92.0 3551 13 ADT8443	XX	PA (LEBY/) LEE Y. B.								
c 18.4 92.0 3678 2 ARV6310	XX	PA (AHC/) AHN C.								
c 18.4 92.0 3678 2 ARV6310	XX	PA (JIAN/) JIANG X.								
c 18.4 92.0 3678 6 AAD38995	XX	PI Yoon H., Mao L., Lee Y.B., Ahn C., Jiang X.								
c 18.4 92.0 3678 6 AAD38995	XX	PX								
c 18.4 92.0 3678 6 AAD38995	XX	DR WPI; 2004-561492/54.								
c 18.4 92.0 3678 6 AAD38995	XX	PT New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in several cancer cells.								
c 18.4 92.0 3678 6 AAD38995	XX	PT Claim 1; SEQ ID NO 2; 35pp; English.								

CC The invention describes a compound, RX-0047 or RX-0149 targeted to a
 CC nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
 CC where the oligonucleotide compound inhibits the expression of human HIF-
 CC 1. Also described are: a method of inhibiting the expression HIF-1 in
 CC human cells or tissues; and a method of inducing cytotoxicity in a cancer
 CC cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
 CC fully defined sequence comprising 20 bp (SEQ ID NO. 20, 5',
 CC atatggccacccgtgtccaa 3', and SEQ ID NO. 4, 5', ggagcttacatccaaatgc 3',
 CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a human HIF-1
 CC antisense oligonucleotide.
 XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATATGGCCACCCGTGTCCAA 20
 Db 1 ATATGGCCACCCGTGTCCAA 20

RESULT 2
 ADQ88721/C
 ID ADQ88721 standard; DNA; 20 BP.
 XX AC ADQ88721;
 XX DT 21-OCT-2004 (first entry)
 XX DE Human hypoxia inducible factor-1 gene fragment seqid 1.
 XX KW RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
 KW cancer; infection; inflammation; tumour formation; ss.
 OS Homo sapiens.
 XX PN US2004152655-A1.
 XX PD 05-AUG-2004.
 XX PR 28-JAN-2004; 2004US-00766185.
 XX PR 31-JAN-2003; 2003US-0444367P.
 XX PR 09-AUG-2001.
 XX PR 17-JAN-2001; 2001WO-US001354.
 XX PR 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-018464P.
 XX PR 02-MAR-2000; 2000US-0186550P.
 XX PR 16-MAR-2000; 2000US-0189814P.
 XX PR 17-MAR-2000; 2000US-0190076P.
 XX PR 18-APR-2000; 2000US-0198123P.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PR 28-JUN-2000; 2000US-0214886P.
 XX PR 30-JUN-2000; 2000US-0215135P.
 XX PR 07-JUL-2000; 2000US-0216880P.
 XX PR 07-JUL-2000; 2000US-0217488P.
 XX PR 11-JUL-2000; 2000US-0217496P.
 XX PR 14-JUL-2000; 2000US-0218290P.
 XX PR 26-JUL-2000; 2000US-0220563P.
 XX PR 14-AUG-2000; 2000US-0224519P.
 XX PR 14-AUG-2000; 2000US-0225213P.
 XX PR 14-AUG-2000; 2000US-0225214P.
 XX PR 14-AUG-2000; 2000US-022566P.
 XX PR 14-AUG-2000; 2000US-022567P.
 XX PR 14-AUG-2000; 2000US-022568P.
 XX PR 14-AUG-2000; 2000US-0225740P.
 XX PR 14-AUG-2000; 2000US-022575P.
 XX PR 14-AUG-2000; 2000US-0225758P.
 XX PR 18-AUG-2000; 2000US-0226779P.
 XX PR 22-AUG-2000; 2000US-0226681P.
 XX PR 22-AUG-2000; 2000US-0226688P.
 XX PR 22-AUG-2000; 2000US-0227182P.

CC respectively). The compounds are useful for inhibiting the expression of
 CC HIF-1 and inducing the cytotoxicity in several cancer cells. The
 CC antisense compounds are also useful for preventing or delaying infection,
 CC inflammation, or tumour formation. This sequence represents a site on the
 CC HIF-1 to which antisense oligonucleotides can be targeted in order to
 CC control HIF-1 gene expression.
 XX Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATATGGCCACCCGTGTCCAA 20
 Db 20 ATATGGCCACCCGTGTCCAA 1

RESULT 3
 AAK7781
 ID AAK7781 standard; DNA; 27884 BP.
 XX AC AAK7781;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32593.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 XX FN WO200157182-A2.
 XX PD 09-AUG-2001.
 XX PR 17-JAN-2001; 2001WO-US001354.
 XX PR 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-018464P.
 XX PR 02-MAR-2000; 2000US-0186550P.
 XX PR 16-MAR-2000; 2000US-0189814P.
 XX PR 17-MAR-2000; 2000US-0190076P.
 XX PR 18-APR-2000; 2000US-0198123P.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PR 28-JUN-2000; 2000US-0214886P.
 XX PR 30-JUN-2000; 2000US-0215135P.
 XX PR 07-JUL-2000; 2000US-0216880P.
 XX PR 07-JUL-2000; 2000US-0217488P.
 XX PR 11-JUL-2000; 2000US-0217496P.
 XX PR 14-JUL-2000; 2000US-0218290P.
 XX PR 26-JUL-2000; 2000US-0220563P.
 XX PR 14-AUG-2000; 2000US-0224519P.
 XX PR 14-AUG-2000; 2000US-0225213P.
 XX PR 14-AUG-2000; 2000US-0225214P.
 XX PR 14-AUG-2000; 2000US-022566P.
 XX PR 14-AUG-2000; 2000US-022567P.
 XX PR 14-AUG-2000; 2000US-022568P.
 XX PR 14-AUG-2000; 2000US-0225740P.
 XX PR 14-AUG-2000; 2000US-022575P.
 XX PR 14-AUG-2000; 2000US-0225758P.
 XX PR 18-AUG-2000; 2000US-0226779P.
 XX PR 22-AUG-2000; 2000US-0226681P.
 XX PR 22-AUG-2000; 2000US-0226688P.
 XX PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 20000US-0227009P. PR 17-NOV-2000; 20000US-0249210P. PR 01-SEP-2000; 20000US-0229287P. PR 01-SEP-2000; 20000US-0229343P. PR 01-SEP-2000; 20000US-022935P. PR 05-SEP-2000; 20000US-022959P. PR 05-SEP-2000; 20000US-022953P. PR 06-SEP-2000; 20000US-0230437P. PR 06-SEP-2000; 20000US-0230438P. PR 08-SEP-2000; 20000US-0231242P. PR 08-SEP-2000; 20000US-0231143P. PR 08-SEP-2000; 20000US-0231124P. PR 08-SEP-2000; 20000US-0231143P. PR 08-SEP-2000; 20000US-0231144P. PR 08-SEP-2000; 20000US-0231208P. PR 08-SEP-2000; 20000US-0231242P. PR 12-SEP-2000; 20000US-0231168P. PR 14-SEP-2000; 20000US-0231297P. PR 14-SEP-2000; 20000US-0231298P. PR 14-SEP-2000; 20000US-0231299P. PR 14-SEP-2000; 20000US-0231414P. PR 08-SEP-2000; 20000US-0231208P. PR 08-SEP-2000; 20000US-0231201P. PR 12-SEP-2000; 20000US-0231168P. PR 14-SEP-2000; 20000US-0231297P. PR 14-SEP-2000; 20000US-0231298P. PR 14-SEP-2000; 20000US-0231299P. PR 14-SEP-2000; 20000US-0231240P. PR 14-SEP-2000; 20000US-0231241P. PR 14-SEP-2000; 20000US-02313063P. PR 14-SEP-2000; 20000US-02313064P. PR 14-SEP-2000; 20000US-02313065P. PR 21-SEP-2000; 20000US-0231223P. PR 21-SEP-2000; 20000US-0231274P. PR 25-SEP-2000; 20000US-0231499P. PR 25-SEP-2000; 20000US-0231998P. PR 26-SEP-2000; 20000US-023184P. PR 27-SEP-2000; 20000US-0231834P. PR 29-SEP-2000; 20000US-0231836P. PR 29-SEP-2000; 20000US-0231827P. PR 29-SEP-2000; 20000US-0231367P. PR 29-SEP-2000; 20000US-0231368P. PR 29-SEP-2000; 20000US-0231369P. PR 29-SEP-2000; 20000US-0231370P. PR 01-OCT-2000; 20000US-0231703P. PR 01-OCT-2000; 20000US-0231038P. PR 02-OCT-2000; 20000US-0231039P. PR 02-OCT-2000; 20000US-0231704P. PR 13-OCT-2000; 20000US-0231935P. PR 20-OCT-2000; 20000US-0231937P. PR 20-OCT-2000; 20000US-0241960P. PR 20-OCT-2000; 20000US-0241221P. PR 20-OCT-2000; 20000US-0241785P. PR 20-OCT-2000; 20000US-0241786P. PR 20-OCT-2000; 20000US-0241787P. PR 20-OCT-2000; 20000US-0241808P. PR 20-OCT-2000; 20000US-0241809P. PR 20-OCT-2000; 20000US-0241826P. PR 01-NOV-2000; 20000US-0246117P. PR 08-NOV-2000; 20000US-02466474P. PR 08-NOV-2000; 20000US-0246475P. PR 08-NOV-2000; 20000US-0246476P. PR 08-NOV-2000; 20000US-0246477P. PR 08-NOV-2000; 20000US-0246528P. PR 08-NOV-2000; 20000US-0246532P. PR 08-NOV-2000; 20000US-0246524P. PR 08-NOV-2000; 20000US-0246525P. PR 08-NOV-2000; 20000US-0246526P. PR 08-NOV-2000; 20000US-0246511P. PR 08-NOV-2000; 20000US-0246512P. PR 08-NOV-2000; 20000US-0246528P. PR 17-NOV-2000; 20000US-0249207P. PR 17-NOV-2000; 20000US-0249208P. PR 17-NOV-2000; 20000US-0249209P.

PR (HUMA-) HUMAN GENOME SCI INC. XX
 PI Rosen CA, Barash SC, Ruben SM; XX
 DR WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
 CC Disclosure; SEQ ID NO 32593; 3071PP + Sequence Listing; English.
 XX
 PT AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM92170 to AAM9321. (I) have cyrostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive protein or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) Proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM92169 represent sequences used in the exemplification of the present invention XX
 SQ Sequence 27884 BP; 9296 A; 5084 C; 5260 G; 8244 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 27884;
 Best Local Similarity 100.0%; Pred. No. 6.2%;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGCCACCTGTGCCAA 20
 Db 1129 ATGGAGCCACCTGTGCCAA 1148

RESULT 4
 ID ADT7841/C
 ID ADT7841 Standard: cDNA: 57500 BP

XX
AC ADN78441;
XX DT 27-JAN-2005 (first entry)
XX DS Human Hif1alpha cDNA sequence #2.
XX KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; Hif1alpha; Hif2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW peroxisome; atherosclerosis; smooth muscle cell proliferation;
KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW ophthalmological; antiinflammatory; respiratory; vasoconstrictor; gene; ss.
XX OS Homo sapiens.
XX PN US2004120393-A1.
XX PD 04-NOV-2004.
XX PR 21-NOV-2003; 2003US-00719370.
XX PR 23-NOV-2002; 2002US-00304126.
XX PA (WARD/) WARD D T.
XX PA (DOBIE/) DOBIE K W.
XX PA (MARC/) MARCUSSON E G.
XX PA (FREIER/) FREIER S M.
PT Ward DR, Dobie KW, Marcusson EG, Freier SM;
DR WPI; 2004-774955/76.
XX PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (Hif1 alpha) and/or Hif2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
PS Example 15: SEQ ID NO 11; 195pp; English.
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (Hif1alpha) and/or
CC hypoxia-inducible factor 2 alpha (Hif2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of Hif1alpha and/or
CC Hif2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5'-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents human Hif1alpha cDNA.
XX SQ sequence 57500 BP; 17058 A; 10565 C; 10922 G; 18956 T; 0 U; 0 Other;
Best Local Similarity 100.0%; Score 20; DB 12; Length 57501;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 54375 ATGGAGGCCACCGATGTGCA 54356
RESULT 6
AX78996 AX78996 standard; DNA; 37 BP.
XX AC NAX78996;
XX DT 17-AUG-1999 (first entry)
DB HIF-alpha gene amplification primer #2.
XX KW Chimeric; transactivator protein; DNA binding domain; HIF; VP16;
KW hypoxia-inducible factor; transcriptional activation; expression vector;
KW normoxic; ischaemic tissue; damage; ss.
OS Synthetic.
OS Homo sapiens.

CC differential expression of the gene indicates at least one toxic effect.
 CC The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect
 CC of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences).

CC Sequence 2711 BP; 798 A; 613 C; 623 G; 677 T; 0 U; 0 Other;
 CC Best Local Similarity 92.0%; Score 18.4%; DB 10; Length 2711;
 CC Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC Oy 1 ATGAGGCCACCGTGTCCA 20
 CC Db 2707 AGTAGGCCACAGTGTCRA 2688

RESULT 9

ABQ5451/c
 ID ABQ5451 standard; cDNA; 2861 BP.
 KK AC ABQ5451;

XX DT 22-AUG-2002 (first entry)

DB Human ovarian antigen HNOR010 cDNA, SEQ ID NO:431.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; neuroprotective; antibody preparation; cytotoxic; immunomodulatory; antiinflammatory; gynaecological; reproductive; chromosome 14q21-24; gene; ss.

XX OS Homo sapiens.
 XX PN WO200200677-A1.
 XX PD 03-JAN-2002.
 XX PR 07-JUN-2001; 2001WO-US018569.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;
 XX DR WPI; 2002-147878/19.
 XX PR -PSDB; ABP41474.

XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

XX PS Claim 1; SEQ ID NO 431; 2922pp; English.

XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymolecules, antibodies against human ovarian antigens, and the use of ovarian antigen polymolecules and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovary or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents DNA encoding a human ovarian antigen of the invention. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences).

RESULT 10

ADU16279/c
 ID ADU16279 standard; DNA; 3203 BP.
 KK AC ADU16279;
 KK DT 22-APR-2004 (first entry)

DB Query Match 92.0%; Score 18.4%; DB 6; Length 2861;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX OS Sequence 2861 BP; 960 A; 539 C; 484 G; 877 T; 0 U; 1 Other;
 XX PN 1 ATGAGGCCACCGTGTCCA 20
 XX PR 1677 AGTAGGCCACAGTGTCRA 1658

RESULT 10

ADU16279/c
 ID ADU16279 standard; DNA; 3203 BP.
 KK AC ADU16279;
 KK DT 22-APR-2004 (first entry)

DE Human nucleic acid-associated protein (NAPP) coding sequence #14.
 KK human; nucleic acid-associated protein; NAPP; autoimmune disorder; inflammatory disorder; AIDS; allergy; infection; metabolic disorder; obesity; reproductive disorder; infertility; neurological disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; myocardial infarction; hypertension; eye disorder; cell proliferative disease; cancer; db; gene.
 KK Homo sapiens.
 XX PN WO2003094848-A2.
 XX PR 20-NOV-2003.
 XX PR 09-MAY-2003; 2003WO-US014450.
 XX PR 10-MAY-2002; 2002US-0379843P.
 PR 24-MAY-2002; 2002US-0384457P.
 PR 31-MAY-2002; 2002US-0384699P.
 PR 06-JUN-2002; 2002US-03897265P.
 XX PA (INCYT-) INCYTE CORP.
 XX PI Kable AB, Elliott VS, Tran UK, Ramkumar J, Marquis JP, Chawla NK; Richardson TW, Bulloch SA, Khare R, Lee SY, Lal PG, Tang YT, Yue H;

PI Swarnkar A, Becha SD, Hafilia AJA, Chang H, Baughn MR, Borowsky ML;
 PI Gietzen KJ, He A, Forsythe JJ, Sprague WM, Blake JJ, Warren BA;
 PI Mason PM, Ison CH, Lindquist EA, Wilson AD, Jin P;
 XX WPI; 2004-01199/01.
 DR P-PSDB; ADA12229.

XX New human nucleic acid associated proteins and polynucleotides, useful
 PT for diagnosing, preventing or treating diseases or conditions associated
 PT with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or
 PT stroke.

XX Claim 5; SEQ ID NO 64; 400pp; English.

CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
 CC the invention are useful in diagnosing, preventing and treating
 CC diseases/conditions associated with altered expression of NAAP, such as:
 CC autoimmune/inflammatory disorders (e.g. AIDS and allergies), infections
 CC (e.g. bacterial and viral), metabolic disorders (e.g. obesity),
 CC reproductive disorders (e.g. infertility), neurological disorders (e.g.
 CC Parkinson's disease and Alzheimer's disease), cardiovascular disorders
 CC (e.g. myocardial infarction and hypertension), eye disorders, or cell
 CC proliferative diseases (e.g. cancer). The present DNA sequence encodes a
 XX human NAAP protein of the invention.

SQ Sequence 3203 BP; 978 A; 691 C; 653 G; 881 T; 0 U; 0 Other;

Query Match	92.0%	Score	18.4	DB	12	Length	3203
Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2766	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 11

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 12

Best Local Similarity	92.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 13

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 14

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 15

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 16

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 17

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 18

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 19

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 20

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 21

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 22

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 23

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 24

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 25

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 26

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 27

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 28

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 29

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 30

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 31

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 32

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 33

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 34

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 35

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 36

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 37

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 38

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 39

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 40

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 41

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 42

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 43

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 44

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 45

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 46

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 47

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 48

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 49

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 50

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 51

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 52

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT 53

Best Local Similarity	95.0%	Pred.	No. 31				
Matches	19	Conservative	0	Mismatches	1	Indels	0
Ov	1	AATCAGGCCACCACTGTCCAA	20				
Db	2794	AGTGTAGCCACCGAGTCCAA	2775				

RESULT

CC ADR25751, producing a protein by culturing the host cell, and a
 CC composition comprising a purified antibody that specifically binds to the
 CC proteins. The foam cell-expressed nucleic acids are useful for a high
 CC throughput detection of differential expression of one or more
 CC polynucleotides in a sample. The sample is from a subject with
 CC atherosclerosis and comparison with a standard defined early, mid or late
 stages of the disorder. The foam cell-expressed nucleic acids are useful
 CC for high throughput screening of a library of molecules or compounds to
 CC identify a ligand which binds
 CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
 CC useful for a high throughput screening of library of molecules or
 CC compounds to identify at least one ligand which specifically binds a
 CC protein, for purifying a ligand from a sample for making a antibody. The
 CC foam cell-expressed nucleic acids are useful for diagnosing cardiovascular
 CC disease. The foam cell-expressed nucleic acids are useful
 CC as elements on a microarray which can be used for detecting related
 CC polymucleotide in a sample, diagnosing cardiovascular disease,
 CC atherosclerosis. The present sequence represents a cDNA whose expression
 CC is upregulated in LPS treated foam cells.

SQ Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;
 XX Best Local Similarity 92.0%; Score 18.4; DB 10; Length 3229;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAGGCCACCACTGTCCA 20
 Db 2794 AGTGAGGCCACCACTGTCCA 2775

RESULT 13
 ADJ5607/c
 ID ADJ5607 standard; cDNA; 3229 BP.
 AC ADJ5607;
 XX DT 06-MAY-2004 (first entry)
 DE Human cDNA differentially expressed in MYCN activated cells seqID 113.
 KW human; differential expression; transactivator; proto-oncogene;
 KW neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;
 KW MYCN activated cell.
 OS Homo sapiens.
 PN US2003119099-A1.
 XX PD 26-JUN-2003.
 XX PR 25-FEB-2002; 2002US-00084817.
 XX PR 23-FEB-2001; 2001US-0270754P.
 XX PR (STUA/) STUART S G.
 PA (NNUCH/) NUCHTERN J G.
 PA (PLON/) PLON S E.
 PA (SHOH/) SHOET J M.
 PT Stuart SG, Nuchtern JG, Plon SE, Shohet JM;
 XX DR WPI; 2003-635698/60.

CC poly nucleotide sequences that exhibit differential expression patterns in
 CC cells activated by the transactivator MYCN, where MYCN is a proto-
 CC oncogene that is amplified in neuroblastoma cells and is common in small
 CC cell lung cancers. The present invention describes these cDNA molecules
 CC as useful for in hybridization assays to detect expression of nucleic
 CC acids (or complementary nucleic acids) in a present in a given sample, as
 CC well as for screening assays by identifying molecules or compounds that
 CC specifically bind the cDNA as a ligand and modulate function or activity.
 Accordingly, these compositions exhibit cytostatic activity and can also
 CC be used for gene therapy purposes. This poly nucleotide sequence is a cDNA
 CC that is differentially expressed in MYCN activated cells, given in an
 exemplification of the invention. Note: This sequence does not appear in
 CC the printed specification but has been obtained in electronic format from
 CC the US Patent Office at
 CC <http://seqdata.uspto.gov/Sequence.html?DocID=20030119009>.
 XX SQ Sequence 3229 BP; 987 A; 695 C; 658 G; 889 T; 0 U; 0 Other;
 XX Best Local Similarity 92.0%; Score 18.4; DB 10; Length 3229;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAGGCCACCACTGTCCA 20
 Do 2794 AGTGAGGCCACCACTGTCCA 2775

RESULT 14
 ADR76983/c
 ID ADR76983 standard; cDNA; 3229 BP.
 AC ADR76983;
 XX DT 29-JAN-2004 (first entry)
 DE Human cDNA differentially expressed in a liver disorder #106.
 KW human; ss; gene; liver disorder; hyperlipidaemia; hypertension;
 KW type II diabetes; tumour; liver; inflammatory disorder;
 KW immune response disorder; high-throughput screening;
 KW differential gene expression; gene therapy.
 OS Homo sapiens.
 PN US2003108871-A1.
 XX PD 12-JUN-2003.
 XX PR 30-JUL-2001; 2001US-00919039.
 XX PR 28-JUL-2000; 2000US-0222113P.
 XX PA (KASE/) KASER M R.
 XX PT Kaser MR;
 XX DR WPI; 2004-031227/03.
 DR P-PSDB; ADR76984.
 XX PT Composition comprising several cDNAs that are differentially expressed in
 PT treated human C3A liver cell cultures, useful for treating liver
 disorders.
 XX PS Claim 1; SEQ ID NO 148; 41pp; English.

CC The invention relates to a composition comprising several cDNAs that are
 CC differentially expressed in a liver disorder. The composition is useful
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type
 CC II diabetes, tumours of the liver and disorders of the inflammatory and
 CC immune response. The composition is useful for a high-throughput method
 CC of screening several molecules or compounds to identify a ligand which
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 CC high-throughput method for using a protein to screen several molecules or

CC compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding and detecting specific binding between the protein and molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents a cDNA differentially expressed in a liver disorder.

XX SQ Sequence 3229 BP; 987 A; 658 G; 889 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 3229;
Best Local Similarity 95.0%; Pred. No. 31; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AATGAGGCCACCACTGTCCAA 20

Db 2794 AGTGAGGCCACCACTGTCCAA 2775

XX SQ Sequence 3551 BP; 1150 A; 671 C; 650 G; 1080 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 12; Length 3551;
Best Local Similarity 95.0%; Pred. No. 31; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AATGAGGCCACCACTGTCCAA 20

Db 2428 AGTGAGGCCACCACTGTCCAA 2409

Search completed: May 21, 2006, 21:17:47
Job time : 261.5 secs

RESULT 15
ADN74945/c
ID ADN74945 standard; cDNA; 3551 BP.
XX AC ADN74945;
XX DT 12-AUG-2004 (first entry)
DE DNA encoding human hypoxia-inducible factor 1 alpha #2.
XX KW ss; gene; human; antisense therapy; hypoxia-inducible factor 1 alpha;
XX hyperproliferative disorder.
OS Homo sapiens.

XX FH key Location/Qualifiers
FT 29. 2236
PT /*tag= A
FT /product= "Hypoxia-inducible factor 1 alpha"
PN US2004101858-A1.
XX PD 27-MAY-2004.
XX PP 23-NOV-2002; 2002US-00304126.
PR 23-NOV-2002; 2002US-00304126.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DR, Doble KW;
PI XE DR WPI: 2004-399686/37.
DR P-PSDB; ADN75066.
XX PT New compounds, particularly oligonucleotides targeted to a nucleic acid encoding hypoxia-inducible factor 1 alpha, useful for treating disease associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative disorders.

XX PS Example 15, SEQ ID NO 13; 80DP; English.

The invention relates to antisense oligonucleotides targeted to, and which specifically hybridize with, and inhibit expression of, a nucleic acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense oligonucleotides are useful for treating a disease or condition associated with hypoxia-inducible factor 1 alpha, such as a hyperproliferative disorder. They are also useful in research and diagnostics for modulating the expression of hypoxia-inducible factor 1 alpha. The present sequence represents DNA encoding human hypoxia-inducible factor 1 alpha #2.

Run on:	May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds (without alignments) 502.985 Million cell updates/sec										
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Post-processing:	Minimum Match 0% Listing first 45 summaries										
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	6: gb_htc:*										
	7: gb_est2:*										
	8: gb_est7:*										
	9: gb_est8:*										
	10: gb_est9:*										
	11: gb_gb1:*										
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	14: gb_gb4:*										
SUMMARIES											
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Result No.	Query Match Length	DB ID	Description								
1	20	238	BR764191	RESULT 1	BB764191	238 bp	mRNA	linear	EST 19-SEP-2000		
2	20	250	BR764172	LOCUS	BB764191	115-NT0071-200600-106-h11 NT0071	Homo sapiens	CDNA, mRNA	sequence.		
3	20	255	CY820845	DEFINITION	BB764191						
4	20	266	BR764166	VERSION	BB764191.1	GI:10194115					
5	20	317	BR718942	KEYWORDS	EST:						
6	20	327	BR160136	SOURCE	Homo sapiens (human)						
7	20	344	DNL130625	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptilgires; Primates; Catarrhini; Homidae; Homo.						
8	20	375	DYL153390	REFERENCE	1 (bases 1 to 238)						
9	20	378	CD288229	AUTHORS	Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagi, M.A., da Silva, W. Jr., Zigo, M.A., Bordin, S., Costa, F.P., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, O'Hare, M.J., Soares, P., Brentani, R.R., Ris, L.F., de Souza, S.J. and Simpson, A.J.						
10	20	389	DYL12562	TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags						
11	20	394	BE7925260	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
12	20	403	CA778645	PUBLMED	10737600						
13	20	492	DYL79093	COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br						
14	20	537	AJ663529	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tit=kt2=ILS-NT0071-2006-05-h11&t2=2000-06-20&t4=1)							
15	20	545	BF923330	SEQ_PRIMER, PUC 18 forward							
16	20	560	CX593021	High quality sequence start: 5'							
17	20	591	DN402969	High quality sequence stop: 238.							
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/db_xref="taxon:9606"
 /dev_stage="Adult"
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 /note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-Tlibrary was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the PUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 238;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 20; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 AATGAGGCCACCAGTGTCCA 20
 db 156 AATGAGGCCACCAGTGTCCA 137

RESULT 2
 BE764172 LOCUS BB764172 250 bp mRNA linear EST 19-SEP-2000
 DEFINITION NT5-NT0071-200600-106-c10 Homo sapiens cDNA, mRNA sequence.
 VERSION BE764172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1. (bases 1 to 250)
 REFERENCE Authors Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=nt2-1L5-NT0071-2006-106-c10&t3=2000-06-20&t4=1>)
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 /mol_type="mRNA"
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 /dev_stage="Adult"
 /clone_lib="NT0071"
 /note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-Tlibrary was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the PUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 250;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAGTGTCCA 20
 db 83 AATGAGGCCACCAGTGTCCA 102

RESULT 3
 CVB26845/C LOCUS CVB26845 brain and spinal cord cDNA library in Gecko Gekko japonicus CDNA clone SJ15D12, mRNA sequence.

DEFINITION EST001143 brain and spinal cord cDNA library in Gecko Gekko japonicus

ACCESSION CVB26845
 VERSION CVB26845.1 GI:55776384
 KEYWORDS EST.
 SOURCE Gekko japonicus
 ORGANISM Gekko japonicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
 REFERENCE 1 (bases 1 to 255)
 AUTHORS Gu, X., Ding, F., Liu, Y., Liu, M., Shen, M., Gong, L., Zhang, Q., Tang, X., and Yang, H.
 TITLE Analysis of expressed sequences tags and cloning of full length cDNA from brain and spinal cord cDNA library in Gecko (2004).
 JOURNAL Unpublished (2004)
 COMMENT Contact: Gu Xiaobong
 The Key Laboratory of Neuroregeneration of Jiangsu Province
 Nantong Medical College
 Qixiu Road 19, Nantong city, Jiangsu Province, P.R.China
 Tel: 86-513-5051800
 Fax: 86-513-5511585
 Email: neurong@public.nt.jb.cn.
 Location/Qualifiers 1..255
 /organism="Gekko japonicus"
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 /clone="SJ15D12"
 /tissue="brain and spinal cord"
 /clone.Lib="brain and spinal cord cDNA library in Gecko"

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 255;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAGTGTCCA 20
 db 234 AATGAGGCCACCAGTGTCCA 215

RESULT 4
 BE764166/C LOCUS BE764166 brain and spinal cDNA, mRNA sequence.

DEFINITION IL5-NT0071-200600-106-D05 NT0071 Homo sapiens

VERSION BE764166
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORP expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBLMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=&l2=MR0-HT0695-0600-001-h08&t3=2000-08-06&t4=1>)
FEATURES Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 317.
 Location/Qualifiers

FEATURES**source****ORIGIN**</div

/mol type="mRNA"
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 /clone_lib="pTR041"
 /note="Organ: head neck; Vector: puc18; Site_1: SmarT;
 Site_2: SmarT; head neck; Vector: puc18; Site_1: SmarT;
 Site_2: SmarT; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 327;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGGCCACAGGTCCA 20
 Db 63 AATGGCCACAGGTCCA 82

RESULT 7
 DN130625 DN130625 344 bp mRNA linear EST 15-FEB-2005
 DEFINITION 1147199 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
 ACCESSION DN130625
 VERSION EST
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Suina; Suidae; Sus.
 1. (bases 1 to 344)
 REFERENCES Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.
 AUTHORS Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross match v0_990339. A column: 11
 Plate: HRY8037 row: A column: 11
 Seq primer: TAGAGGCCAGTCGAGG.

JOURNAL
 COMMENT
 FEATURES source 1..344
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="MARC 4PIG"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4PIG"
 /note="Vector: pCDNA1.1; Site_1: EcoRI; Site_2: NotI;
 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."
 ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 344;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGGCCACAGGTCCA 20
 Db 98 AATGGCCACAGGTCCA 117

RESULT 8
 DY153390/c LOCUS DY153390
 DEFINITION 00705BMPA002625HT BMPA Bos taurus CDNA, mRNA sequence.
 ACCESSION 00705BMPA002625HT BMPA
 VERSION DY153390.1 GI:86347565
 KEYWORDS EST
 SOURCE Bos taurus (cattle)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1. (bases 1 to 375)
 REFERENCES McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S., Glenn,M., Havukka,I., Watson,J., Crawford,A., Wheeler,T., Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macpbool,N., McMahon,C., McCracken,J., Stelwagen,K., Parr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whiteley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEvans,J. and Atkinson,P.
 AUTHORS AgResearch, Genesis and Primary Industry Victoria Bovine EST project
 TITLE Unpublished (2006)
 JOURNAL Contact: Macpbool N
 COMMENT AgResearch Ltd.
 Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand
 FEATURES source 1..375
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pre-Partum mammary"
 /clone_lib="BMPA"
 /note="Vector: PBK-CMV; Bovine 85 days pre-partum mammary tissue cDNA library derived from tissue harvested from an Angus cow by Adrian Molenaar on 01/01/00"
 ORIGIN Query Match 100.0%; Score 20; DB 10; Length 375;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGGCCACAGGTGCCAA 20
 Db 78 AATGGCCACAGGTGCCAA 59

RESULT 9
 CD288229/c LOCUS CD288229
 DEFINITION 3..113..abd POE14 (Day_14_pregnant_ovine_endometrium) Ovis aries
 ACCESSION CD288229
 VERSION CD288229.1 GI:31086272
 KEYWORDS EST
 SOURCE Ovis aries (sheep)
 ORGANISM Ovis aries
 1. (bases 1 to 378)
 REFERENCES Gray,C.A., Abbey,C.A., Beremand,P.D., Choi,Y., Farmer,J.L., Adelson,D.J., Thomas,T.L., Bazer,F.W. and Spencer,T.B.
 AUTHORS Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
 TITLE Identification of Endometrial Genes Regulated by Early Pregnancy, Progesterone, and Interferon Tau in the Ovine Uterus
 JOURNAL Biol. Reprod.
 COMMENT 1651498
 Contact: Thomas E. Spencer
 Center for Animal Biotechnology and Genomics
 Texas A&M University
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471.

USA
Tel: 9798454896
Fax: 9798622662
Email: tspancer@ansc.tamu.edu.
FEATURES
Source
Location/Qualifiers
1. .378
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/sex="Female"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
/clone_lib="POB14 (Day 14 pregnant ovine endometrium)"
/note="Organ: uterus; Vector: TripleX2; Site 1: EcoRI;
Site 2: XbaI; Non-normalized library, sequenced 5, with
TripleX2 primer (CTCCGAGATCGACAGC). Library constructed
by Clontech with total RNA extracted using the Trizol
method and pooled from 5 females."
ORIGIN
Query Match 100.0%; Score 20; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; N mismatches 0; Gaps 0;
Qy 1 AATGAGGCCACCAAGTCCAA 20
Db 351 AATGAGGCCACCAAGTCCAA 332
RESULT 10
DY112562.c
LOCUS DY112562
DEFINITION 000222BOVB005432HT BOVb
ACCESSION DY112562
VERSION 1
KEYWORDS EST
ORGANISM Bos taurus (cattle)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1.(bases 1 to 389)
REFERENCE
AUTHORS McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn.M., Hawukkala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macbool,N., McMahon,C.,
Nicholaus,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McSwan,J. and
Atkinson,P.
TITLE AgResearch, Genesis and Primary Industry Victoria Bovine EST
Project
JOURNAL Unpublished (2006)
COMMENT Contact: Macbool N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
Mossie, New Zealand
Email: nauman.macbool@agresearch.co.nz.
FEATURES
source
Location/Qualifiers
1. .389
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Ovarian"
/clone_lib="BOVB"
/note="Vector: DBK-CMV; Bovine ovary cDNA library derived
from tissue harvested from an unknown breed calf by Allian
Crawford on 28/09/99"
ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; N mismatches 0; Gaps 0;
Qy 1 AATGAGGCCACCAAGTCCAA 20
Db 89 AATGAGGCCACCAAGTCCAA 108
RESULT 11
Qy 1 AATGGCCACCAAGTCCAA 20
Db 152 AATGAGGCCACCAAGTCCAA 133
RESULT 11
LOCUS BB925260
DEFINITION CM4-An0081-210800-274-d01 AN0081 Homo sapiens cDNA, mRNA sequence.
ACCESSION BB925260
VERSION BB925260.1
KEYWORDS EST
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 394)
AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva W. Jr., Zago,M.A., Bordim,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
Simpson,A.J.
TITLE shotgun sequencing of the human transcriptome with ORF expressed
SEQUENCE TAGS Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 1073700
PUBMED 1073700
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: askimpson@ludwig.org.br
This sequence was derived from the PAPBSP/LICR Human Cancer Genome
Project. This entry can be seen in the PAPBSP/LICR Human Cancer Genome
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=et2=CM4-AN0081-210
80-274-d01&t3=200-08-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 392.
Location/Qualifier 1.
1..394
/note="Organ: amniotic fluid; Vector: puc18;
Site 2: Small; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research),
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 394;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; N mismatches 0; Gaps 0;
Qy 1 AATGAGGCCACCAAGTCCAA 20
Db 89 AATGAGGCCACCAAGTCCAA 108
RESULT 12
LOCUS CA778645/c
DEFINITION MPL38410_D22 MPL Sub scrofa cDNA clone psport15 , mRNA sequence.
ACCESSION CA778645

VERSION CR778645.1 GI:26016521
 KEYWORD EST
 SOURCE Sub scrofa (pig)
 ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 SUBS.
 REFERENCES (bases 1 to 403)
 AUTHORS Center for Animal Functional Genomics.
 JOURNAL Generation of ESTs from mixed pig cDNA libraries
 COMMENT Unpublished (2002)
 Contact: Steven P. Suchyta
 Center for Animal Functional Genomics, Department of Animal Science
 Michigan State University
 B215 Anthony Hall, East Lansing, MI 48824, USA
 Tel: 517 355 8443
 Fax: 517 432 9168
 Email: suchytas@msu.edu
 Single Pass sequencing. Bases called and alt-trimmed with phred v0.0204425.c. Vector identified by cross_match with the -minscore 20 -minmatch 12 options.
 Seq Primer: T7.

FEATURES source
 Location/Qualifiers
 1..403
 /organism="Sub scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:823"
 /clone="PSORTI"
 /sex="Male"
 /tissue_type="pooled"
 /dev_stage="pooled"
 /lab="host:"DH10B"
 /clone_lib="MPL"
 /note="Organ: pooled; Vector: PSORTI; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from adipose, adrenal gland, blood leukocytes, brain, cartilage, eye, heart, intestine, kidney, liver, lung, lymph nodes, mammary gland, myogenic satellite cells, ovary, pancreas, pituitary gland, placenta, skin, spinal cord, spleen, stomach, tendon, testes, uterus, and vascular from various developmental and physiological stages."
 ORIGIN
 Query Match 100.0% Score 20; DB 4; Length 403;
 Best Local Similarity 100.0% Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 216 AATGAGCCACCAAGTGTCCA 197

RESULT 13
 LOCUS DV769093/C
 DEFINITION ILLUMIGEN MCQ_67822 Katze MMTR Macaca mulatta cDNA clone BIOW3915_5' similar to Bases 5 to 392 highly similar to human HIF1A (HS_509554), mRNA sequence.
 VERSION DV769093.1
 EST. GI:82613035
 SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 REFERENCES 1 (bases 1 to 492)
 AUTHORS Magnes, C.I., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Fitzgibbon, M., Miner, D.G., Katze, M.G. and Iadonato, S.P.
 TITLE Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human

JOURNAL Genome Biol. 6 (7), R60 (2005)
 PUBLISHED 1599449
 COMMENT Contact: C. Magnes
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnes@illumigen.com
 Sequenced on 2005-08-01. 669 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org
 PCR PRIMERS FORWARD: CCCTCACTAAAGGGACAAA
 BACKWARD: CACTATGGCGAATTGGCTTA
 Insert Length: 492 Std Error: 0.00
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 Seq primer: CCCTCACAAAGGGACAAAA
 POLY(A)=No.
 FEATURES source
 Location/Qualifiers
 1..492
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="indian"
 /db_xref="taxon:9544"
 /clone="IBI0W39154"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="juvenile"
 /lab_host="Electromax DH10B"
 /clone_lab="Katze MMTR"
 /note="Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I; Created from CloneMiner cdNA Library Construction kit (catalog #18249-029)"
 ORIGIN
 Query Match 100.0% Score 20; DB 10; Length 492;
 Best Local Similarity 100.0% Pred. No. 70;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 417 AATGAGCCACCAAGTGTCCA 398

RESULT 14
 LOCUS AJ683529/C
 DEFINITION AJ683529 CSEQRAN04 Sub scrofa cDNA clone C0001802_F15, mRNA
 SOURCE AJ683529 Sequence.
 ORGANISM Sub scrofa (pig)
 ACCESSION AJ683529 EST.
 KEYWORDS Sub scrofa (pig)
 JOURNAL Sub scrofa (pig)
 COMMENT 1 (bases 1 to 537)
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 JOURNAL Unpublished (2004)
 CONTACT Anderson, S.I.
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.2045.c. Vector identified by cross-match with the -minscore 20 and -minmatch 12 options. Vector: pBluescriptII (KS+) R. Site: EcorI R. Site2: NotI 5'. Seq Primer: M13P Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

FEATURES EH25 9 pbs, www.arkogenomics.org.
 source Location/Qualifiers
 1. .537
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C001802_F15"
 /tissue type="uterus"
 /clone_lib="CSEQRAN04"
 /note="Vector: pb18ScriptII_ks+; Site_1: EcoRI; Site_2:
 NotI; Single pass sequencing, Normalised library
 constructed from pig uterus."
 ORIGIN
 Query Match 100.0%; Score 20; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATGAGCCACCAAGTCCAA 20
 Db 214 AATGAGCCACCAAGTCCAA 195
 RESULT 15
 BF923330 545 bp mRNA linear EST 19-JAN-2001
 LOCUS FR2-NT0137-211100-005-a08 NT0137 Homo sapiens cDNA, mRNA Sequence.
 DEFINITION BF923330.1 GI:12319218
 ACCESSION BF923330.1
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Organism
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Rhachontoglires; Primates; Catarrhini;
 Homidae; Homo
 REFERENCES 1 (bases 1 to 545)
 AUTHORS Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
 Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., de oliveira, P.S., Bucher, P., Joncuzzi, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAEPSS/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pit1=MR2&c2=MR2-NT0137-211100-005-a08&c3=2000-11-21&t=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 543.
 FEATURES Location/Qualifiers
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 1. .545
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0137"
 /note="Organ: nervous tumor; Vector: puc18; Site_1: Small;
 Site_2: Small; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the PUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:18:10 ; Search time 79.5 Seconds (without alignments)

470.719 Million cell updates/sec

Title: US-10-766-185-2

Sequence: 1 aatgaccacgtgtccaa 20

Scoring table: IDENTITY_NUC Gapop 10.0 - Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB_seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB_seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/8 COMB_seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/9 PCTUS COMB_seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB_seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RB COMB_seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

Result No.	Score	Query Match	Length	DB ID	Description
c 1	19.6	100.0	601	3 US-09-949-016-22571	Sequence 22571, A
c 2	19.6	100.0	601	3 US-09-949-016-52342	Sequence 52342, A
c 3	18.4	92.0	3678	3 US-09-949-016-8797-2	Sequence 2, Appli
c 4	18.4	92.0	311	3 US-09-949-016-17247	Sequence 17247, A
c 5	18.4	92.0	601	3 US-09-949-016-22570	Sequence 22570, A
c 6	18.4	92.0	601	3 US-09-949-016-52341	Sequence 52341, A
c 7	18.4	92.0	2770	3 US-09-949-016-1518	Sequence 1518, Appli
c 8	18.4	92.0	3229	3 US-09-949-016-148	Sequence 148, Appli
c 9	18.4	92.0	3678	3 US-09-949-016-662-22	Sequence 22, Appli
c 10	18.4	92.0	3678	3 US-09-949-016-873B-19	Sequence 19, Appli
c 11	18.4	92.0	3678	3 US-09-949-016-158-22	Sequence 22, Appli
c 12	18.4	92.0	3736	2 US-08-080-413B-1	Sequence 1, Appli
c 13	18.4	92.0	3736	3 US-08-915-213-1	Sequence 1, Appli
c 14	18.4	92.0	3736	3 US-09-148-547-1	Sequence 1, Appli
c 15	18.4	92.0	3736	3 US-09-235-217-1	Sequence 1, Appli
c 16	18.4	92.0	3736	3 US-09-283-581-1	Sequence 1, Appli
c 17	18.4	92.0	3736	7 PCT-US86-102051-21	Sequence 1, Appli
c 18	18.4	92.0	3933	3 US-09-949-016-1218	Sequence 1, Appli
c 19	18.4	92.0	18120	3 US-09-949-016-13460	Sequence 13460, A
c 20	18.4	92.0	56714	3 US-09-949-016-11960	Sequence 11960, A
c 21	16.4	82.0	3924	3 US-09-023-655-1168	Sequence 1168, Appli
c 22	16.4	82.0	3924	3 US-09-162-195-2	Sequence 2, Appli
c 23	16.4	82.0	3924	4 US-09-080-107-2299	Sequence 2299, Appli

Alignments

RESULT 1

US-09-949-016-22571/c

; Sequence 22571, Application US/09949016

; Patent No. 6812319

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09-949-016-115100

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60-241755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60-237768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60-231498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 22571

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-22571

Query Match 100.0%; Score 20; DB 3; Length 601;

Best Local Similarity 95.0%; Pred. No. 1.2;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGACCCACCAAGTGTCCAA 20

:|||||:|||||:|||||:|||||:|||

Db 302 ARTGACCCACCAAGTGTCCAA 283

RESULT 2

US-09-949-016-52342/c

; Sequence 52342, Application US/09949016

; Patent No. 6812319

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09-949-016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60-241755

PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 52342
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-52342

Query Match 100.0%; Score 20; DB 3; Length 601;
 Best Local Similarity 95.0%; Pred. No. 1.;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCAA 20
 Db 302 AATGAGCCACCAAGTGTCAA 283

RESULT 3
 US-09-579-897-2
 Sequence 2, Application US/09579897
 Patent No. 6432927
 GENERAL INFORMATION:
 APPLICANT: Gregory, Richard
 APPLICANT: Vincent, Karen
 TITLE OF INVENTION: Compositions and Methods for Inducing Gene Expression
 FILE REFERENCE: GA0112CIP2
 CURRENT APPLICATION NUMBER: US/09/579,897
 CURRENT FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/067,546
 PRIOR FILING DATE: 1997-12-04
 PRIOR APPLICATION NUMBER: PCT/US98/25753
 PRIOR FILING DATE: 1998-12-04
 PRIOR APPLICATION NUMBER: 09/133,612
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 2
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-579-897-2

Query Match 92.0%; Score 18.4%; DB 3; Length 37;
 Best Local Similarity 95.0%; Pred. No. 3.;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCAA 20
 Db 8 AATGAGCCACCAAGTGTCAA 27

RESULT 4
 US-09-621-976-17247/C
 Sequence 17247, Application US/09621976
 Patent No. 6639063
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J.B.
 APPLICANT: Jober, S.
 APPLICANT: Giordano, J.Y.
 TITLE OF INVENTION: ESTR8 and Encoded Human Proteins.
 FILE REFERENCE: GENSET 054PR2
 CURRENT APPLICATION NUMBER: US/09/621,976
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SOFTWARE: Patent.pm
 SEQ ID NO: 17247
 LENGTH: 311
 TYPE: DNA

Query Match 92.0%; Score 18.4%; DB 3; Length 601;
 Best Local Similarity 95.0%; Pred. No. 5.2;

Qy 1 AATGAGCCACCAAGTGTCAA 20
 Db 198 AATGAGCCACCAAGTGTCAA 179

RESULT 5
 US-09-949-016-22570/c
 Sequence 22570, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 22570
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-22570

Query Match 92.0%; Score 18.4%; DB 3; Length 601;
 Best Local Similarity 95.0%; Pred. No. 5.2;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCAA 20
 Db 597 AATGAGCCACCAAGTGTCAA 578

RESULT 6
 US-09-949-016-52341/C
 Sequence 52341, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 52341
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-52341
 Query Match 92.0%; Score 18.4%; DB 3; Length 601;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 597 AGTGAACCAACAGTGTCAA 578

RESULT 7
 US-09-949-016-1518/c
 Sequence 1118, Application US/0949016
 GENERAL INFORMATION:
 | APPLICANT: VENTER, J. Craig et al.
 | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 | FILE REFERENCE: CLO1307
 | CURRENT APPLICATION NUMBER: US/09/949,016
 | CURRENT FILING DATE: 2000-04-14
 | PRIOR APPLICATION NUMBER: 60/241,755
 | PRIOR FILING DATE: 2000-10-20
 | PRIOR APPLICATION NUMBER: 60/237,768
 | PRIOR FILING DATE: 2000-10-03
 | PRIOR APPLICATION NUMBER: 60/231,498
 | PRIOR FILING DATE: 2000-09-08
 | SOFTWARE: FastSEQ for Windows Version 4.0
 | SEQ ID NO 1518
 | LENGTH: 2770
 | TYPE: DNA
 | ORGANISM: Human
 US-09-949-016-1518

Query Match 92.0%; Score 18.4; DB 3; Length 2770;
 Best Local Similarity 95.0%; Pred. No. 6.5;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 1647 AGTGAACCAACAGTGTCAA 1628

RESULT 8
 US-09-919-039-148/c
 Sequence 148, Application US/0919039
 GENERAL INFORMATION:
 | APPLICANT: Kaser, Matthew R.
 | TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CBLL CULTURES
 | FILE REFERENCE: PA-0035 US
 | CURRENT APPLICATION NUMBER: US/09/919,039
 | CURRENT FILING DATE: 2002-09-09
 | PRIOR APPLICATION NUMBER: 60/222,113
 | PRIOR FILING DATE: 2000-07-28
 | NUMBER OF SEQ ID NOS: 401
 | SOFTWARE: PBRL Program
 | SEQ ID NO 148
 | LENGTH: 3229
 | TYPE: DNA
 | ORGANISM: Homo sapiens
 | FEATURE: misc_feature
 | OTHER INFORMATION: Incyte ID No. 6727066 1250434CB1
 US-09-919-039-148

Query Match 92.0%; Score 18.4; DB 3; Length 3229;
 Best Local Similarity 95.0%; Pred. No. 6.6;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 2794 ACTGAGCCACCAAGTGTCCA 2775

RESULT 9
 US-09-380-662-22/c
 Sequence 22, Application US/09380662
 | Patent No. 6376199
 | GENERAL INFORMATION:
 | APPLICANT: Caniglia, Isabella
 | APPLICANT: Post, Martin
 | APPLICANT: Lye, Stephen
 | TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
 | FILE REFERENCE: 11757.38USWO
 | CURRENT APPLICATION NUMBER: US/09/380,662
 | CURRENT FILING DATE: 1999-12-21
 | PRIOR APPLICATION NUMBER: PCT/CA98/00180
 | PRIOR FILING DATE: 1998-03-05
 | PRIOR APPLICATION NUMBER: US 60/039,919
 | SEQ ID NO 22
 | SOFTWARE: PatentIn version 3.0
 | LENGTH: 3678
 | TYPE: DNA
 | ORGANISM: Homo sapiens
 | FEATURE: CDS
 | NAME/KEY: CDS
 | LOCATION: (29). (2509)
 US-09-380-662-22

Query Match 92.0%; Score 18.4; DB 3; Length 3678;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 2555 AGTGAACCAACAGTGTCAA 2536

RESULT 10
 US-09-959-873B-19/c
 Sequence 19, Application US/09959873B
 | Patent No. 6787326
 | GENERAL INFORMATION:
 | APPLICANT: Ratcliffe, Peter John
 | APPLICANT: Maxwell, Patrick Henry
 | APPLICANT: Pugh, Christopher William
 | TITLE OF INVENTION: Interaction Between the VHL Tumour Suppressor and Hypoxia Inducible Factor, and Assay Methods
 | FILE REFERENCE: 3547.1.000-000
 | CURRENT APPLICATION NUMBER: US/09/959,873B
 | CURRENT FILING DATE: 2001-11-09
 | PRIOR APPLICATION NUMBER: PCT/G800/0826
 | PRIOR FILING DATE: 2000-05-12
 | PRIOR APPLICATION NUMBER: GB9911047.0
 | PRIOR FILING DATE: 1999-05-12
 | NUMBER OF SEQ ID NOS: 19
 | SOFTWARE: FastSEQ for Windows Version 4.0
 | SEQ ID NO 19
 | LENGTH: 3678
 | TYPE: DNA
 | ORGANISM: Homo sapiens
 US-09-959-873B-19

Query Match 92.0%; Score 18.4; DB 3; Length 3678;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 20
 Db 2555 AGTGAACCAACAGTGTCAA 2536

RESULT 11
 US-10-028-158-22/c

Sequence 22, Application US/10028158
 ; Patent No. 6863980
 ; GENERAL INFORMATION:
 ; APPLICANT: Caniggia, Isabella
 ; APPLICANT: Post, Martin
 ; APPLICANT: Lye, Stephen
 ; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
 ; FILE REFERENCE: 11757.380SWO
 ; CURRENT FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US/10/028,158
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: PCT/CA98/00180
 ; PRIOR FILING DATE: 1998-03-05
 ; PRIOR FILING DATE: 1997-03-07
 ; NUMBER OF SEQ ID NOs: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 22
 ; LENGTH: 3678
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (29)...(2509)
 ; US-10-028-158-22

Query Match 92.0%; Score 18.4%; DB 3; Length 3678;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCATGTGCCAA 20
 Db 2555 AGTGAGCCACCATGTGCCAA 2536

RESULT 13
 US-08-915-213-1/c
 ; Sequence 1, Application US/08915213
 ; Patent No. 6030462
 ; GENERAL INFORMATION:
 ; APPLICANT: Semenza, Gregg L.
 ; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/915,213
 ; FILING DATE: 20-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,473
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/053001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3736 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-915-213-1/c

Query Match 92.0%; Score 18.4%; DB 3; Length 3736;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCATGTGCCAA 20
 Db 2555 AGTGAGCCACCATGTGCCAA 2536

RESULT 14
 US-03-148-547-1/c
 ; Sequence 1, Application US/09148547
 ; Patent No. 6124131
 ; GENERAL INFORMATION:
 ; APPLICANT: Semenza, Gregg L.
 ; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
 ; FILE REFERENCE: 07265/151001

REGISTRATION NUMBER: 38,347
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3736 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

CURRENT APPLICATION NUMBER: US/09/148,547
 CURRENT FILING DATE: 1998-08-25
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 1
 LENGTH: 3736
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (29) .. (2509)
 US-09-148-547-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATGAGGCCACCAGGTCCAA 20
 Db 2555 AGTGAAGCCACCAGGTCCAA 2536

RESULT 15

US-09-235-217-1/C
 Sequence 1, Application US/09235217
 Patent No. 6222018
 GENERAL INFORMATION:
 APPLICANT: Semenza, Gregg L.
 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 NUMBER OF SEQUENCES: 64
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/235,217
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/480,473
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Halle, Lisa A.
 REFERENCE/DOCKET NUMBER: 38-347
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 619/678-5070
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3736 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-235-217-1

Query Match 92.0%; Score 18.4; DB 3; Length 3736;
 Best Local Similarity 95.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATGAGGCCACCAGGTCCAA 20
 Db 2555 AGTGAAGCCACCAGGTCCAA 2536

Search completed: May 21, 2006, 21:21:00
 Job time : 81.5 secs

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Om nucleic - nucleic search, using bw model.

Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds
 (without alignments)

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatggccaccaggctccaa 20

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 3778434

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_Main.*

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 2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq/*
 3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09A_PUBCOMB.seq/*
 4: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09B_PUBCOMB.seq/*
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 10: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10E_PUBCOMB.seq/*
 11: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10F_PUBCOMB.seq/*
 12: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10G_PUBCOMB.seq/*
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 14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11B_PUBCOMB.seq/*
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 16: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11D_PUBCOMB.seq/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-10-766-185-1/c

; Sequence 1, Application US/10766185
 ; Publication No. US20040152655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yoon, Heejeong
 ; APPLICANT: Ahn, Chang Ho
 ; APPLICANT: Lee, Young Bok
 ; APPLICANT: Mao, Lingjun
 ; APPLICANT: Jiang, Xiaoming
 ; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
 ; CURRENT APPLICATION NUMBER: US/10/766,185
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 130
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: human
 US-10-766-185-1

Query Match Best Local Similarity Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCGTGTCAA 20
 Db 20 ATGAGCCACCAAGTGTCAA 1

RESULT 2

US-10-766-185-2

; Sequence 2, Application US/10766185
 ; Publication No. US20040152655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yoon, Heejeong
 ; APPLICANT: Ahn, Chang Ho
 ; APPLICANT: Lee, Young Bok
 ; APPLICANT: Mao, Lingjun

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
c 1	20	100.0	20 8 US-10-766-185-1	Sequence 1, Appli
c 2	20	100.0	8 US-10-766-185-2	Sequence 2, Appli
c 3	20	100.0	57200 9 US-10-719-370A-11	Sequence 11, Appli
c 4	20	100.0	57501 8 US-10-304-126-11	Sequence 11, Appli
c 5	19.6	100.0	1558 4 US-09-925-063A-706976	Sequence 706976,
c 6	19.6	100.0	1558 5 US-09-925-063A-706976	Sequence 706976,
c 7	18.4	92.0	37 6 US-10-190-394-2	Sequence 2, Appli
c 8	18.4	92.0	375 8 US-10-242-532A-41677	Sequence 41677, A
c 9	18.4	92.0	375 8 US-10-085-783A-41677	Sequence 41677, A
c 10	18.4	92.0	1400 10 US-10-264-049-431	Sequence 5878, Ap
c 11	18.4	92.0	2861 7 US-10-125-784-3	Sequence 3, Appli
c 12	18.4	92.0	3180 7 US-10-045-817-113	Sequence 148, Appli
c 13	18.4	92.0	3229 3 US-09-919-039-148	Sequence 148, Appli
c 14	18.4	92.0	3229 6 US-10-208-408-22	Sequence 22, Appli
c 15	18.4	92.0	3229 6 US-10-084-817-113	Sequence 113, Appli
c 16	18.4	92.0	3229 7 US-10-247-67-19	Sequence 19, Appli
c 17	18.4	92.0	3551 8 US-10-304-126-13	Sequence 13, Appli

1 APPLICANT: Jiang, Xiaoming
 1 TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
 1 FILE REFERENCE: REX 7034
 1 CURRENT APPLICATION NUMBER: US10/766,185
 1 CURRENT FILING DATE: 2004-01-28
 1 NUMBER OF SEQ ID NOS: 130
 1 SOFTWARE: PatentIn version 3.1
 1 SEQ ID NO: 2
 1 LENGTH: 20
 1 TYPE: DNA
 1 ORGANISM: artificial sequence
 1 FEATURE:
 1 OTHER INFORMATION: antisense oligonucleotide
 US-10-766-185-2

Query Match 100.0%; Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCAA 20
 Db 1 AATGAGGCCACCAAGTGTCCAA 20

RESULT 3
 US-10-719-370A-11/c
 Sequence 11, Application US10719370A
 Publication No. US20040220393A1.
 GENERAL INFORMATION:
 1 APPLICANT: Ward, Donna T.
 1 APPLICANT: Dobie, Kenneth W.
 1 APPLICANT: Marcusson, Eric G.
 1 APPLICANT: Freier, Susan M.
 1 TITLE OF INVENTION: MODULATION OF HIF1A AND HIF2A EXPRESSION
 1 FILE REFERENCE: ISPT-1010
 1 CURRENT APPLICATION NUMBER: US10/719,370A
 1 CURRENT FILING DATE: 2003-11-21
 1 PRIOR APPLICATION NUMBER: US 10/304,126
 1 PRIOR FILING DATE: 2002-11-23
 1 NUMBER OF SEQ ID NOS: 458
 1 SOFTWARE: PatentIn version 3.2
 1 SEQ ID NO: 11
 1 LENGTH: 57500
 1 TYPE: DNA
 1 ORGANISM: Homo sapiens
 1 FEATURE:
 1 NAME/KEY: misc_feature
 1 LOCATION: (1)..(57500)
 1 OTHER INFORMATION: positions 82000 to 139500 of the sequence with GenBank Accession
 1 PUBLICACION INFORMATION:
 1 DATABASE ACCESSION NUMBER: AL137129.4
 1 DATABASE ENTRY DATE: 2001-04-30
 1 RELEVANT RESIDUES: (1)..(57500)
 US-10-719-370A-11

Query Match 100.0%; Score 20; DB 9; Length 57500;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCAA 20
 Db 54374 AATGAGGCCACCAAGTGTCCAA 54355

RESULT 4
 US-10-304-126-11/c
 Sequence 11, Application US10304126
 Publication No. US20040101855A1
 GENERAL INFORMATION:
 1 APPLICANT: Ward, Kenneth W.
 1 APPLICANT: Dobie, Kenneth W.
 1 TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION

Query Match 100.0%; Score 20; DB 8; Length 57501;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCAA 20
 Db 54375 AATGAGGCCACCAAGTGTCCAA 54356

RESULT 5
 US-09-925-065A-706976/c
 Sequence 706976, Application US/09925065A
 Publication No. US20040181048A1
 GENERAL INFORMATION:
 1 APPLICANT: Wang, David G.
 1 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 1 FILE REFERENCE: 108827.135
 1 CURRENT APPLICATION NUMBER: US/09/925,065A
 1 CURRENT FILING DATE: 2001-08-08
 1 PRIOR APPLICATION NUMBER: US 60/243,096
 1 PRIOR FILING DATE: 2000-10-24
 1 PRIOR APPLICATION NUMBER: US 60/252,147
 1 PRIOR FILING DATE: 2000-11-20
 1 PRIOR APPLICATION NUMBER: US 60/250,092
 1 PRIOR FILING DATE: 2000-11-30
 1 PRIOR APPLICATION NUMBER: US 60/261,766
 1 PRIOR FILING DATE: 2001-01-16
 1 PRIOR APPLICATION NUMBER: US 60/289,846
 1 PRIOR FILING DATE: 2001-05-09
 1 NUMBER OF SEQ ID NOS: 957056
 1 SOFTWARE: FastSEQ for Windows Version 4.0
 1 SEQ ID NO: 706976
 1 LENGTH: 1558
 1 TYPE: DNA
 1 ORGANISM: Homo sapiens
 US-09-925-065A-706976

Query Match 100.0%; Score 20; DB 4; Length 1558;
 Best Local Similarity 95.0%; Pred. No. 8.2;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCAA 20
 Db 33 AATGAGGCCACCAAGTGTCCAA 14

RESULT 6
 US-09-925-065A-706976/c
 Sequence 706976, Application US/09925065A
 Publication No. US20040228172A9
 GENERAL INFORMATION:
 1 APPLICANT: Wang, David G.
 1 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 1 FILE REFERENCE: 108827.135
 1 CURRENT APPLICATION NUMBER: US/09/925,065A
 1 CURRENT FILING DATE: 2001-08-08
 1 PRIOR APPLICATION NUMBER: US 60/243,096
 1 PRIOR FILING DATE: 2000-10-24
 1 PRIOR APPLICATION NUMBER: US 60/252,147
 1 PRIOR FILING DATE: 2000-11-20
 1 PRIOR APPLICATION NUMBER: US 60/250,092
 1 PRIOR FILING DATE: 2000-11-30
 1 PRIOR APPLICATION NUMBER: US 60/261,766
 1 PRIOR FILING DATE: 2001-01-16
 1 PRIOR APPLICATION NUMBER: US 60/289,846
 1 PRIOR FILING DATE: 2001-05-09
 1 NUMBER OF SEQ ID NOS: 957056
 1 SOFTWARE: FastSEQ for Windows Version 4.0
 1 SEQ ID NO: 706976
 1 LENGTH: 1558
 1 TYPE: DNA
 1 ORGANISM: Homo sapiens
 US-09-925-065A-706976

Query Match 100.0%; Score 20; DB 4; Length 1558;
 Best Local Similarity 95.0%; Pred. No. 8.2;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCAA 20
 Db 33 AATGAGGCCACCAAGTGTCCAA 14

```

; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 951086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 706976
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-063A-706976

Query Match          100.0%; Score 20; DB 5; Length 1558;
Best Local Similarity 95.0%; Pred. No. 8.2%;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGNGTCCAA 20
Db      33 ARTGAGGCCACCAGTGTCCAA 14

RESULT 7
US-10-190-394-2
; Sequence 2, Application US/10190394
; Publication No. US20030018007A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; INVENTION: Compositions and Methods for Inducing Gene Expression
; TITLE OF INVENTION: Expression
; FILE REFERENCE: GAO112CIP2
; CURRENT APPLICATION NUMBER: US/10/190,394
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/579,897
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/067,546
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/25753
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/133,612
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-190-394-2

Query Match          92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGTGTCCAA 20
Db      8 AGTGAGGCCACCAGTGTCCAA 27

RESULT 8
US-10-242-535A-41677/c
; Sequence 41677, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; INVENTION: Compositions and Methods Relating to Osteoarthritis
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 41677
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-41677

Query Match          92.0%; Score 18.4; DB 8; Length 375;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGTGTCCAA 20
Db      165 AGTGAGGCCACCAGTGTCCAA 146

RESULT 9
US-10-085-783A-41677/c
; Sequence 41677, Application US/10085783A
; Publication No. US20040017841A1
; GENERAL INFORMATION:
; APPLICANT: Lieuw, C.C.
; INVENTION: Compositions and Methods Relating to Osteoarthritis
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 41677
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-41677

Query Match          92.0%; Score 18.4; DB 8; Length 375;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGTGTCCAA 20
Db      165 AGTGAGGCCACCAGTGTCCAA 146

RESULT 10
US-10-956-157-5878/c
; Sequence 5878, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 10081)
; CURRENT APPLICATION NUMBER: US 10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5878
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Human
; US-10-956-157-5878/c

Query Match          92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGTGTCCAA 20
Db      8 AGTGAGGCCACCAGTGTCCAA 27

RESULT 11
US-10-956-157-5878/c
; Sequence 5878, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 10081)
; CURRENT APPLICATION NUMBER: US 10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5878
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Human
; US-10-956-157-5878/c

Query Match          92.0%; Score 18.4; DB 6; Length 37;
Best Local Similarity 95.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AATGAGGCCACCAGTGTCCAA 20
Db      8 AGTGAGGCCACCAGTGTCCAA 27

```

Organism: Homo sapiens
US-10-936-157-5878

Query Match Score 92.0%; Pred. No. 34; DB 10; Length 1400;
Best Local Similarity 95.0%;保守性 0; Mismatches 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; SEQ ID NO: 3

Qy 1 AATGAGGCCACCAGTGTCCAA 20
Db 258 AGTGAGGCCACCAGTGTCCAA 239

RESULT 11
US-10-264-049-431/C
Sequence 431, Application US/10264049
GENERAL INFORMATION:
PUBLICATION NO. US20040005579A1

APPLICANT: BiTE et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264, 049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4160
SEQ ID NO: 431
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2853) . (2853)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

Query Match Score 92.0%; Pred. No. 35; DB 7; Length 2861;
Best Local Similarity 95.0%;保守性 0; Mismatches 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; SEQ ID NO: 3

Qy 1 AATGAGGCCACCAGTGTCCAA 20
Db 1677 AGTGAGGCCACCAGTGTCCAA 1658

RESULT 12
US-10-425-784-3/C
Sequence 3, Application US/10425784
Publication No. US2004000959A1

GENERAL INFORMATION:
APPLICANT: Comer, Allen
APPLICANT: Hoffmann, Michael
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth Factors
FILE REFERENCE: STRATA-08110
CURRENT APPLICATION NUMBER: US/10/425, 784
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 60/376, 488
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 3
LENGTH: 3180
TYPE: DNA
ORGANISM: Homo sapiens
US-10-425-784-3

Query Match Score 92.0%; Pred. No. 36; DB 7; Length 3180;
Best Local Similarity 95.0%;保守性 0; Mismatches 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; SEQ ID NO: 3

Qy 1 AATGAGGCCACCAGTGTCCAA 20
Db 2794 AGTGAGGCCACCAGTGTCCAA 2775

RESULT 13
US-09-919-039-148/C
Sequence 148, Application US/09919039
Publication No. US2003010887A1

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELLS CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919, 039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222, 113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO: 148
LENGTH: 3229
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2003010887A1 1250434CB1
US-09-919-039-148

Query Match Score 92.0%; Pred. No. 36; DB 7; Length 3229;
Best Local Similarity 95.0%;保守性 0; Mismatches 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; SEQ ID NO: 3

Qy 1 AATGAGGCCACCAGTGTCCAA 20
Db 2794 AGTGAGGCCACCAGTGTCCAA 2775

RESULT 14
US-10-208-408-22/C
Sequence 22, Application US/10208408
Publication No. US20030096272A1

GENERAL INFORMATION:
APPLICANT: Scheibe, Xiao Min
TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
FILE REFERENCE: PA-0048-1 US
CURRENT APPLICATION NUMBER: US/10/208, 408
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 60/308, 868
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO: 22
LENGTH: 3229
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CB1
US-10-208-408-22

Query Match Score 92.0%; Pred. No. 36; DB 6; Length 3229;
Best Local Similarity 95.0%;保守性 0; Mismatches 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; SEQ ID NO: 3

Qy 1 AATGAGGCCACCAGTGTCCAA 20
Db 2794 AGTGAGGCCACCAGTGTCCAA 2775

RESULT 15
US-10-084-817-113/C
Sequence 113, Application US/10084817
Publication No. US20030119009A1

GENERAL INFORMATION:
| APPLICANT: Susan Stuart
| APPLICANT: Jed G. Muchtern
| APPLICANT: Sharon E. Plon
| TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
| FILE REFERENCE: PA-0046 US
| CURRENT APPLICATION NUMBER: US/10/084,817
| CURRENT FILING DATE: 2002-02-25
| PRIOR APPLICATION NUMBER: 60/270,784
| PRIOR FILING DATE: 2001-02-23
| NUMBER OF SEQ ID NOS: 365
| SOFTWARE: PERL Program
| SEQ ID NO: 113
| LENGTH: 3229
| TYPE: DNA
| ORGANISM: Homo sapiens
| FEATURE:
| NAME/KEY: misc feature
| OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1.
us-10-084-61-113

Query Match 92.0%; Score 18 4; DB 6; Length 3229;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AATGAGCCCAAGGTCCA 20
Db 2794 AGTGAGCCACCAAGTCCAA 2775

Search completed: May 21, 2006, 21:48:58
Job time : 85 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 Seconds
(without alignments)
104.527 Million cell updates/sec

Title: US-10-766-185-2

Perfect score: 20

Sequence: 1 aatgaccacgtgtccaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 3527956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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 2: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US06_NEW_PUB.seq:
 3: /EMC_Celerra_SIDS3/prodata/2/pubnpna/US07_NEW_PUB.seq:
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 5: /EMC_Celerra_SIDS3/prodata/2/pubnpna/PCT_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	15.2	76.0	6327	7	US-11-217-529-75787		Sequence 75787, A
c	2	14.2	71.0	25	US-11-217-529-13735		Sequence 13735, A
c	3	14.2	71.0	163	US-11-301-554-1491		Sequence 1491, AP
c	4	14.2	71.0	166	US-11-301-554-1493		Sequence 1393, AP
c	5	14.2	71.0	166	US-11-301-554-1442		Sequence 1442, AP
c	6	14.2	71.0	196	US-11-301-554-125		Sequence 125, APP
c	7	14.2	71.0	422	US-11-301-554-1725		Sequence 1795, AP
c	8	14.2	71.0	638	US-11-301-554-1283		Sequence 1283, AP
c	9	14.2	71.0	663	US-11-301-554-1283		Sequence 710, APP
c	10	14.2	71.0	1041	US-11-301-554-21		Sequence 21, APP1
c	11	14.2	71.0	4600	US-11-301-554-1797		Sequence 1797, AP
c	12	14.2	71.0	394191	US-10-506-549-3		Sequence 3, APP1
c	13	13.8	69.0	244	US-10-488-619-1090		Sequence 1090, AP
c	14	13.8	69.0	2081	US-10-505-928-764		Sequence 764, APP
c	15	13.8	69.0	3127	US-10-196-749-83		Sequence 83, APP1
c	16	13.8	69.0	17569	US-11-301-554-1804		Sequence 1804, AP
c	17	13.6	68.0	192	US-11-217-529-174455		Sequence 174455,
c	18	13.6	68.0	396	US-11-175-7698		Sequence 7698, A
c	19	13.6	68.0	438	US-11-217-529-78028		Sequence 78028, A
c	20	13.6	68.0	468	US-10-488-619-821		Sequence 821, APP
c	21	13.6	68.0	711	US-11-217-529-4803		Sequence 4803, APP
c	22	13.6	68.0	1446	US-11-217-529-76480		Sequence 76480, A
c	23	13.6	68.0	1506	US-11-217-529-81781		Sequence 81781, A
c	24	13.6	68.0	1749	US-11-217-529-2467		Sequence 2267, APP
c	25	13.6	68.0	2379	US-11-217-529-79342		Sequence 79342, A

ALIGNMENTS

RESULT 1
US-11-217-529-75787
 ; Sequence 75787, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAMURA, YOSHIHIRO
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11-217-529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 75787
 ; LENGTH: 6327
 ; TYPE: DNA; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-75787

RESULT 2
US-11-217-529-13735/C
 ; Sequence 13735, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAMURA, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIWA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217-529

CURRENT FILING DATE: 2005-09-02
 / PRIORITY APPLICATION NUMBER: US 10/932,182
 / PRIOR FILING DATE: 2004-09-02
 / NUMBER OF SEQ ID NOS: 197023
 / SOFTWARE: Patentin version 3.3
 / SEQ ID NO: 13735
 / LENGTH: 25

/ TYPE: DNA
 / ORGANISM: *Saccharomyces pastorianus*

US-11-217-329-13735
 Query Match Score 71.0%;保守性 84.2%; DB 7; Length 25;
 Best Local Similarity 84.2%; Pred. No. 21;
 Matches 16, Conservative 0; Mismatches 3;
 Qy 1 AATGAGGCCACCACTGTCCA 19
 Db 24 ACTGAGGCCACAGTGTCAA 6

RESULT 3

US-11-301-554-1491
 / Sequence 14_91, Application US/11301554
 / Publication No. US-0060088527A1

GENERAL INFORMATION:

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Wang, Tongrong

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121_478C21

CURRENT APPLICATION NUMBER: US/11/301,554

CURRENT FILING DATE: 2005-12-13

PRIOR APPLICATION NUMBER: US 10/283,017

PRIOR FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 09/849,872

PRIOR FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US 10/017,754

PRIOR FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: US 09/902,941

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 09/849,626

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: US 09/736,457

PRIOR FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: US 09/702,705

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US 09/677,419

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: US 09/671,325

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 09/658,824

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: US 09/849,626

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: US 09/671,325

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 09/658,824

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US 09/677,419

PRIOR FILING DATE: 2000-10-08

PRIOR APPLICATION NUMBER: US 09/658,824

PRIOR FILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: US 09/671,325

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 09/658,824

PRIOR FILING DATE: 2000-10-08

Best Local Similarity 84.2%; Pred. No. 31;
 Matches 16, Conservative 0; Mismatches 3;
 Qy 1 AATGAGGCCACCACTGTCCA 19
 Db 69 AACCTGCCACAGTGTCCA 87

RESULT 4

US-11-301-554-1393/C
 / Sequence 1393, Application US/11301554
 / Publication No. US20060088527A1

GENERAL INFORMATION:

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Wang, Tongrong

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

/ APPLICANT: Carter, Darrick

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Durham, Margarita

Best Local Similarity 84.2%; Pred. No. 31;
 Matches 16, Conservative 0; Mismatches 3;
 Qy 1 AATGAGGCCACCACTGTCCA 19
 Db 69 AACCTGCCACAGTGTCCA 87

RESULT 5

US-11-301-554-1442
 / Sequence 1442, Application US/11301554
 / Publication No. US20060088527A1

Query Match Score 71.0%;保守性 84.2%; DB 7; Length 166;

Best Local Similarity 84.2%; Pred. No. 31;

Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO: 1393

SOFTWARE: PastSeq for Windows Version 4.0

LENGTH: 166

TYPE: DNA

ORGANISM: Homo sapiens

Query Match Score 71.0%;保守性 84.2%; DB 7; Length 166;

Best Local Similarity 84.2%; Pred. No. 31;

Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO: 2157

SOFTWARE: PastSeq for Windows Version 4.0

LENGTH: 163

TYPE: DNA

ORGANISM: Homo sapiens

Query Match Score 71.0%;保守性 84.2%; DB 7; Length 166;

Best Local Similarity 84.2%; Pred. No. 31;

Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO: 1491

SOFTWARE: PastSeq for Windows Version 4.0

LENGTH: 163

TYPE: DNA

ORGANISM: Homo sapiens

```

; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PAI
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1442
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1442

Query Match Score 14.2; DB 7; Length 166;
Best Local Similarity 84.2%; Prod. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
1 AATGAGGCCACCATGTGCCA 19
2 AACCTGCCAACAGTGTCCA 90

; RESULT 6
US-11-301-554-125
; Sequence 125 Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.

```

```

; / APPLICANT: Bangur, Chaitanya S.
; / APPLICANT: McNabb, Andria
; / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; / TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; / FILE REFERENCE: 210121-478C21
; / CURRENT APPLICATION NUMBER: US/11/301,554
; / CURRENT FILING DATE: 2005-12-13
; / PRIOR APPLICATION NUMBER: US 10/283,017
; / PRIOR FILING DATE: 2002-10-28
; / PRIOR APPLICATION NUMBER: US 10/113,872
; / PRIOR FILING DATE: 2002-03-28
; / PRIOR APPLICATION NUMBER: US 10/017,754
; / PRIOR FILING DATE: 2001-10-29
; / PRIOR APPLICATION NUMBER: US 09/902,941
; / PRIOR FILING DATE: 2001-07-10
; / PRIOR APPLICATION NUMBER: US 09/849,626
; / PRIOR FILING DATE: 2001-05-03
; / PRIOR APPLICATION NUMBER: US 09/736,457
; / PRIOR FILING DATE: 2000-12-13
; / PRIOR APPLICATION NUMBER: US 09/702,705
; / PRIOR FILING DATE: 2000-10-30
; / PRIOR APPLICATION NUMBER: US 09/677,419
; / PRIOR FILING DATE: 2000-10-06
; / PRIOR APPLICATION NUMBER: US 09/671,325
; / PRIOR FILING DATE: 2000-09-26
; / PRIOR APPLICATION NUMBER: US 09/658,824
; / PRIOR FILING DATE: 2000-09-08
; / Remaining Prior Application data removed - See File Wrapper
; / NUMBER OF SEQ ID NOS: 2157
; / SOFTWARE: BlastSEQ For Windows Version 4.0
; / SEQ ID NO 125
; / LENGTH: 196
; / TYPE: DNA
; / ORGANISM: Homo sapiens
US-11-301-554-125

Query Match Similarity 71.0%; Score 14.2%; DB 7; Length 196
Best Local Similarity 84.2%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 3; Indels 3

Qy   1 AATGAGGCCACACTGTCCA 19
Db   102 AACCTGCCACACTGTCCA 120

RESULT 7
US-11-301-554-1795/c
Sequence 1795, Application US/11/301554
Publication No. US20060088527A1
GENERAL INFORMATION:
; / APPLICANT: Henderson, Robert A.
; / APPLICANT: Wang, Tongqiang
; / APPLICANT: Watanabe, Yoshihiro
; / APPLICANT: Kalos, Michael D.
; / APPLICANT: Sleath, Paul R.
; / APPLICANT: Johnson, Jeffrey C.
; / APPLICANT: Retter, Marc W.
; / APPLICANT: Durham, Margarita
; / APPLICANT: Carter, Derrick
; / APPLICANT: Panger, Gary R.
; / APPLICANT: Vedwick, Thomas S.
; / APPLICANT: Bangur, Chaitanya S.
; / APPLICANT: McNabb, Andria
; / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; / TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; / FILE REFERENCE: 210121-478C21
; / CURRENT APPLICATION NUMBER: US/11/301,554
; / CURRENT FILING DATE: 2005-12-13
; / PRIOR APPLICATION NUMBER: US 10/283,017
; / PRIOR FILING DATE: 2002-10-28
; / PRIOR APPLICATION NUMBER: US 10/113,872
; / PRIOR FILING DATE: 00/02-03-18
; / PRIOR APPLICATION NUMBER: US 10/017,754

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; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1283
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ ID: 11-301-554-1283
; Query Match Score 14.2; DB 7; Length 638;
; Best Local Similarity 84.2%; Pred. No. 41;
; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATGAGCCACCAAGTGTCCA 19
Db 389 AACCTGCCACCAAGTGTCCA 371

RESULT 9
US-11-217-529-710/c
; Sequence 710, Application US/11217529
; Publication No. US200601099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197033
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 710
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; SEQ ID: 11-217-529-710

Qy 1 AATGAGCCACCAAGTGTCCA 19
Db 316 ACTGAGCCACCAAGTGTCCA 298

RESULT 10
US-11-301-924-21
; Sequence 21, Application US/11301924
; Publication No. US200601090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhanya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 3148USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13

Qy 1 AATGAGCCACCAAGTGTCCA 19
Db 316 ACTGAGCCACCAAGTGTCCA 298

RESULT 11
US-11-301-924-21
; Sequence 21, Application US/11301924
; Publication No. US200601090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhanya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 3148USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13

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PRIOR APPLICATION NUMBER: US/09/896,186
 PRIOR FILING DATE: 2001-07-29
 PRIOR APPLICATION NUMBER: 60/322,202
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 1041
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 US-11-301-924-21

Query Match 71.0%; Score 14.2%; DB 7; Length 1041;
 Best Local Similarity 84.2%; Prod. No. 45;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCA 19
 Db 49 AATGAGGCCACCAAGTGTCCA 67

RESULT 11
 US-11-301-554-1797
 Sequence 1797, Application US/11301554
 GENERAL INFORMATION:
 APPLICANT: Henderson, Robert A.
 APPLICANT: Wang, Tongtong
 APPLICANT: Watanabe, Yoshihiro
 APPLICANT: Kalos, Michael D.
 APPLICANT: Sleath, Paul R.
 APPLICANT: Johnson, Jeffrey C.
 APPLICANT: Retter, Marc W.
 APPLICANT: Durham, Margarita
 APPLICANT: Carter, Darrick
 APPLICANT: Panger, Gary R.
 APPLICANT: Vednick, Thomas S.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: McNabb, Andria
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210121_478C21
 CURRENT FILING DATE: 2005-12-13
 PRIOR APPLICATION NUMBER: US/11/301,554
 PRIOR FILING DATE: 2002-10-08
 PRIOR APPLICATION NUMBER: US 10/113,872
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 10/017,754
 PRIOR FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: US 09/902,941
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: US 09/849,626
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: US 09/736,457
 PRIOR FILING DATE: 2000-12-13
 PRIOR APPLICATION NUMBER: US 09/702,705
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: US 09/677,419
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: US 09/671,325
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: US 09/658,824
 PRIOR FILING DATE: 2000-09-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 2157
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1797
 LENGTH: 4600
 TYPE: DNA
 ORGANISM: *Homo sapiens*
 US-11-301-554-1797

Query Match 71.0%; Score 14.2%; DB 7; Length 4600;
 Best Local Similarity 84.2%; Prod. No. 61;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATGAGGCCACCAAGTGTCCA 19
 Db 3767 AACCTTGCCACCAAGTGTCCA 3785

RESULT 12
 US-10-506-549-3/C
 Sequence 3, Application US/10506549
 GENERAL INFORMATION:
 APPLICANT: APPLERA CORPORATION
 TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 NUCLEAR ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 TITLE OF INVENTION: AND USES THEREOF?
 FILE REFERENCE: CL001361-US
 CURRENT APPLICATION NUMBER: US/10/506,549
 CURRENT FILING DATE: 2004-09-03
 PRIOR APPLICATION NUMBER: 60/361,343
 PRIOR FILING DATE: 2002-03-05
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 394191
 TYPE: DNA
 ORGANISM: *Homo sapiens*
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)..(394191)
 OTHER INFORMATION: n = A,T,C or G

US-10-506-549-3
 Query Match 71.0%; Score 14.2%; DB 6; Length 394191;
 Best Local Similarity 84.2%; Prod. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ATGAGGCCACCAAGTGTCCA 20
 Db 130263 ATGAGGCCACAGGGCCA 130245

RESULT 13
 US-10-488-619-1090
 Sequence 1090, Application US/10488619
 GENERAL INFORMATION:
 APPLICANT: Greenlee, Winner and Sullivan, P.C.
 TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
 FILE REFERENCE: 98-01_WO
 CURRENT APPLICATION NUMBER: US/10/488,619
 NUMBER OF SEQ ID NOS: 3040
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1090
 LENGTH: 244
 TYPE: DNA
 ORGANISM: *Mus musculus*
 US-10-488-619-1090

Query Match 69.0%; Score 13.8%; DB 6; Length 244;
 Best Local Similarity 88.2%; Prod. No. 55;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCCACCAAGTGTCCA 19
 Db 95 TGAGGCCACCAACTGCCCA 111

RESULT 14

US-10-505-928-764
 ; Sequence 764, Application US/10505928
 ; Publication No. US2006008853241
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505,928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/1505,928
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 764
 ; LENGTH: 2081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-505-928-764

Query Match 69.0%; Score 13.8; DB 6; Length 3127;
 Best Local Similarity 88.2%; Pred. No. 92;
 Matches 15; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 4 GAGCCACCATGTGTCGA 20
 Db 1417 GTGCCACGATGTGTCGA 1401

Search completed: May 21, 2006, 21:34:21
 Job time : 14.5 secs

Query Match 69.0%; Score 13.8; DB 6; Length 2081;
 Best Local Similarity 88.2%; Pred. No. 84;
 Matches 15; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 3 TGAAGCCACCATGTGTCGA 19
 Db 1596 TGAAGCCACCATGTGTCGA 1612

RESULT 15
 US-10-196-749-83/c
 ; Sequence 83, Application US/10196749
 ; Publication No. US200600948641
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Chen,Tian
 ; APPLICANT: Desnoyers,Luc
 ; APPLICANT: Goddard,Audrey
 ; APPLICANT: Godowski,Paul J.
 ; APPLICANT: Gurney,Austin L.
 ; APPLICANT: Pan,James S
 ; APPLICANT: Smith,Victoria
 ; APPLICANT: Watanabe,Colin K.
 ; APPLICANT: Wood,William I.
 ; APPLICANT: Zhang,Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P330R1C340
 ; CURRENT APPLICATION NUMBER: US/10/196,749
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/053263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 83
 ; LENGTH: 3127

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OM nucleic - nucleic search, using sw model.

Run on: May 21, 2006, 21:34:32 ; Search time 1030.5 Seconds
(without alignments)
1241.095 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaggtaaacatctccaaatgc 20

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : GenBank:
1: gb_env:
2: gb_dat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:
9: gb_un:
10: gb_vl:
11: gb_ov:
12: gb_hgt:
13: gb_in:
14: gb_om:
15: gb_ba:

SUMMARIES

No.	Score	Query Length	Match Length	DB ID	Description
1	20	100.0	49	BD187062	BD187062 Polypeptide
2	16	80.0	16	AX927927	AX927927 Sequence
3	15.2	76.0	21	DD159257	DD159257 Primer for
4	14	70.0	49	BD187064	BD187064 Polypeptide
c	5	13.6	68.0	AR119846	AR119846 Sequence
c	6	13.6	68.0	AX077752	AX077752 Sequence
c	7	13.6	68.0	AR119858	AR119858 Sequence
c	8	13.6	68.0	AX077751	AX077751 Sequence
c	9	13.6	68.0	AX18106	AX18106 Sequence
c	10	13.6	68.0	AR119859	AR119859 Sequence
c	11	13.6	68.0	AX224363	AX224363 Sequence
c	12	13.4	67.0	AR312573	AR312573 Sequence
c	13	13.4	67.0	A25211	A25211 Inter-Alu S
c	14	13.4	67.0	E09139	E09139 Synthetic DNA
c	15	13	65.0	A24719	A24719 Primer 2065
c	16	13	65.0	A24722	A24722 primer 2070
c	17	12.8	64.0	AR640085	AR640085 Sequence
c	18	12.8	64.0	AR640086	AR640086 Sequence

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	LOCUS	DEFINITION	LINEAR	PAT
1	BD187062	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.	49 bp	17-JUN-2003
	ACCESION	BD187062		
	VERSION	BD187062.1	GI:31079262	
	KEYWORDS	WO 02099104-A/22.		
	SOURCE	synthetic construct		
	ORGANISM	synthetic construct		
	REFERENCE	other sequences; artificial sequences.		
	AUTHORS	1 (bases 1 to 49)		
	TITLE	Hirayama, M., Kondo, S., and Harada, H.		
	JOURNAL	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.		
	COMMENT	Patent: WO 02099104-A 22 DEC-2002;		
	ORIGIN	POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAYAMA, SHINAE KONDO, HIROSHI HARADA		
	OS	Artificial Sequence		
	PN	WO 02099104-A/22		
	PD	12-DBC-2002		
	PP	04-JUN-2002	WO 2002JP005482	
	PR	05-JUN-2001	JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI	
	PC	C12N5/09, C12Q1/68, C07K14/47, C07K19/00		
	CC	Description of Artificial Sequence: synthetic DNA PH		
	FT	Location/Qualifiers		
	FT	source 1..49 /organism='Artificial Sequence'.		
	FEATURES	Location/Qualifiers		
	source	1..49 /organism="synthetic construct"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:32230"		
	ORIGIN			
	Query Match	100.0%	Score 20;	DB 2;
		Best Local Similarity 100.0%	Pred. No. 17;	Length 49;
		Matches 20;	Conservative 0;	Gaps 0;
			Indels 0;	
			Mismatches 0;	
				Qy

Query Match 100.0% Score 20; DB 2; Length 49;
Best Local Similarity 100.0% Pred. No. 17;
Matches 20; Conservative 0; Gaps 0;
Indels 0; Mismatches 0;

Qy

1 GGAGCTAACATCTCCAGTC 20

Db 26 GGAGCTAACATCTCCAAGTC 45

RESULT 2
AX927927
LOCUS Sequence 13 from Patent WO03088110.
DEFINITION 16 bp DNA
ACCESSION AX927927
VERSION GI:40250734
KEYWORDS synthetic construct
SOURCE
ORGANISM synthetic construct
REFERENCE 1. Thru C.A., h G.A.M. and Kristjansen, P.E.
AUTHORS Oligonucleic compounds for the modulation hif-1alpha expression
TITLE Patent: WO 03085110-A 13 16-Oct-2003;
JOURNAL Cureon A/S (DK)
FEATURES Location/Qualifiers
 source 1..16
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: antisense
oligonucleotide to human HIP-1a"
ORIGIN

Query Match Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1..8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCAAGT 19
Db 1 GCTAACATCTCCAAGT 16

RESULT 3
DD159257
LOCUS Primer for detecting human enterobacteria.
DEFINITION 21 bp DNA linear
ACCESSION DD159257
VERSION GI:83957554
KEYWORDS
SOURCE
ORGANISM unidentified
REFERENCE 1. (bases 1 to 21)
AUTHORS Watanabe, K., Fujimoto, J. and Matsuki, T.
TITLE Primer for detecting human enterobacteria
JOURNAL Patent: JP 2005124495-A 33 19-MAY-2005;
COMMENT OS Designed primer based on 16S rRNA of human enterobacteria
JP 2005124495-A/33
PD 19-NAY-2005
PP 24-OCT-2003 JP 2003364198
PI koichi watanabe, junji fujimoto, takahiro matsuki CC
FH Key
FEATURES Location/Qualifiers
 source 1..21
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
ORIGIN

Query Match Score 15.2; DB 2; Length 21;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 2 GAGCTAACATCTCCAAGTC 21
33 GGAGCTAACATCTCCAAGTC 14

RESULT 4
BD187064
LOCUS BD187064
DEFINITION Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.
ACCESSION BD187064
VERSION GI:31879264
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1. (bases 1 to 49)
AUTHORS Hiraoka, M., Kondo, S. and Harada, H.
TITLE Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.
JOURNAL Patent: WO 02099104-A 24 12-DEC-2002;
POLA CHEMICAL INDUSTRIES INC.,MASAHIRO HIRAKA, SHINAE KONDO, HIROSHI HARADA
COMMENT OS Artificial Sequence
 source PN WO 02099104-A/24
 /organism="artificial sequence"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
ORIGIN

Query Match Score 14; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e-04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTC 14
Db 35 GGAGCTAACATCTC 48

RESULT 5
AR119846/c
LOCUS AR119846
DEFINITION Sequence 19 from patent US 6153421.
ACCESSION AR119846
VERSION AR119846.1 GI:14102545
KEYWORDS
SOURCE Unknown
ORGANISM Unclassified
REFERENCE 1. (bases 1 to 40)
AUTHORS Yanagi, M., Buhk, J., Emerson, S.U. and Purcell, R.H.
TITLE Cloned genomes of infectious hepatitis C viruses and uses thereof
JOURNAL Patent: US 6153421-A 19 28-Nov-2000;
FEATURES Location/Qualifiers
 source 1..40
 /organism="unknown"
 /mol_type="unassigned DNA"
ORIGIN

Query Match Score 13.6; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 33 GGAGCTAACATCTCCAAGTC 14

RESULT 6
AX07752/C AX07752 Sequence 18 from Patent WO0106008. DNA linear PAT 22-FEB-2001
LOCUS DEFINITION Sequence 18 from Patent WO0106008.
ACCESSION AX07752
VERSION AX07752.1 GI:13157648
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Singh,S., Inamdar,A., Ullman,R.P., Cao,L. and Albagli,D.
JOURNAL Multiplexed strand displacement for nucleic acid determinations
FEATURES Patent: WO 0106008-A 18 JAN 2001;
source Aclara Biosciences, Inc. (US)
KEYWORDS Location/Qualifiers
1. .40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="n=6-(biotinamido)hexyl probe"

ORIGIN

Query Match 68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04; DB 2; Length 41;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 26 GGACCTCAAGTCAACAGTC 7

RESULT 7
AR119858 AR119858 Sequence 50 from patent US 6153421. DNA linear PAT 16-MAY-2001
LOCUS DEFINITION Sequence 50 from patent US 6153421.
ACCESSION AR119858
VERSION AR119858.1 GI:14102557
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yanagi,M., Bukh,J., Emerson,S.U. and Purcell,R.H.
JOURNAL Cloned genomes of infectious hepatitis C viruses and uses thereof
FEATURES Patent: US 6153421-A 50 NOV-2000;
source Location/Qualifiers
1..41
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04; DB 2; Length 41;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 8 GGAGCTAACATCTCCAAGTC 27

RESULT 8
AX07751 AX07751 Sequence 17 from Patent WO0106008. DNA linear PAT 22-FEB-2001
LOCUS DEFINITION Sequence 17 from Patent WO0106008.
ACCESSION AX07751
VERSION AX07751.1 GI:13157647
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Singh,S., Inamdar,A., Ullman,R.P., Cao,L. and Albagli,D.
JOURNAL Multiplexed strand displacement for nucleic acid determinations
FEATURES Patent: WO 0106008-A 17 JAN 2001;
source Aclara Biosciences, Inc. (US)
KEYWORDS Location/Qualifiers
1. .41
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="n=6-(biotinamido)hexyl probe"

ORIGIN

Query Match 68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04; DB 2; Length 41;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 16 GGACCTCAAGTCAACAGTC 35

RESULT 9
AX518106/C AX518106/C Sequence 4304 from Patent WO02052044. DNA linear PAT 05-OCT-2002
LOCUS DEFINITION AX518106 from Patent WO02052044.
ACCESSION AX518106
VERSION AX518106.1 GI:23567425
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominoidea; Homo.

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
JOURNAL Detection of genetic polymorphisms
FEATURES Patent: WO 02052044-A 4304 04-JUL-2002;
source Riken (JP)
KEYWORDS Location/Qualifiers
1. .41
/organism="Homo sapiens"
/mol_type="unassigned DNA"

ORIGIN

Query Match 68.0%; Score 13.6; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 4e+04; DB 2; Length 41;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 27 GAAGCTAACATCTCCAAGTC 8

RESULT 10
AR119859 AR119859 Sequence 51 from Patent US 6153421. DNA linear PAT 16-MAY-2001
LOCUS DEFINITION AR119859 from Patent US 6153421.
ACCESSION AR119859
VERSION AR119859.1 GI:14102558
KEYWORDS Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yanagi,M., Bukh,J., Emerson,S.U. and Purcell,R.H.
JOURNAL Cloned genomes of infectious hepatitis C viruses and uses thereof
FEATURES Patent: US 6153421-A 51 NOV-2000;
source Location/Qualifiers
1..42

/organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match Score 13.6; DB 2; Length 42;
 Best Local Similarity 80.0%; Pred. No. 4.1e+04;
 Matches 16; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
 Db 8 GGAGCTAACACTCCAGGCC 27

RESULT 11

LOCUS AX224363 Sequence 7 from Patent WO0161041. DNA linear PAT 10-SEP-2001
 DEFINITION AX224363
 ACCESSION AX224363.1 GI:15554615
 VERSION .
 KEYWORDS Synthetic construct
 SOURCE
 ORGANISM Synthetic construct
 OTHER SEQUENCES: artificial sequences.
 REFERENCE 1. Sharat,S., Cao,L., Hooper,H.H., Albagli,D., Anderson,R. and Zeng,S.
 AUTHORS
 TITLE Multiple-site reaction device and method
 JOURNAL Patent: WO 0161041-A 7 23-AUG-2001;
 Aclara Biosciences, Inc. (US)
 FEATURES 1..42
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="probe"
 misc_feature 41
 /note="n = triethylenglycol"
 misc_feature 42
 /note="n = biotinTEG"
 ORIGIN

Query Match Score 13.6; DB 2; Length 42;
 Best Local Similarity 80.0%; Pred. No. 4.1e+04;
 Matches 16; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
 Db 15 GGACCTCAGCTTACAGTC 34

RESULT 12

LOCUS AR312573 Sequence 3110 from patent US 6559294. DNA linear PAT 12-JUN-2003
 DEFINITION AR312573
 ACCESSION AR312573.1 GI:31705999
 VERSION .
 KEYWORDS Unknown.
 SOURCE Unclassified.
 ORGANISM Unclassified.
 REFERENCE 1. (bases 1 to 20)
 AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
 Sankaran,B. and Fletcher,L.D.
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof
 JOURNAL Patent: US 6559294-A 3110 06-MAY-2003;
 Genent, S.A.; RX;
 FEATURES 1..20
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match Score 13.4; DB 2; Length 20;

Best Local Similarity 93.3%; Pred. No. 4.5e+04;
 Matches 14; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCAG 18
 Db 6 GCTGACATCTCCAG 20

RESULT 13

LOCUS A25211/C
 DEFINITION inter-Alu specific primer DNA (517) from patent WO9213101.
 ACCESSION A25211
 VERSION A25211.1 GI:904591
 KEYWORDS synthetic construct
 SOURCE
 ORGANISM Synthetic construct
 OTHER SEQUENCES: artificial sequences.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS
 TITLE METHOD OF DETECTING DNA SEQUENCE VARIATION
 JOURNAL Patent: WO 9213101-A 2 06-AUG-1992;
 FEATURES Location/Qualifiers
 source 1..27
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 ORIGIN

Query Match Score 13.4; DB 2; Length 27;
 Best Local Similarity 73.7%; Pred. No. 4.7e+04;
 Matches 14; Conservative 2; Mismatches 3;
 Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAGTC 20
 Db 20 GAGCTAACATCTCCAGTC 2

RESULT 14

LOCUS E09139/C
 DEFINITION Synthetic DNA for Alu specific primer.
 ACCESSION E09139
 VERSION E09139.1 GI:22025765
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified sequences.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Andoreau,H.A. and Yan,F.
 TITLE DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
 JOURNAL COMMENT OS None
 INGANII BV
 Parent: JP 1995115999-A 2 09-MAY-1995;
 OS Artificial Sequences.
 OC JP 1995115999-A/2
 PD 09-MAY-1995
 PP 22-MAY-1995 JP 1992130668
 PI ANDREAU HEDAROUSSA ALTSUTERURINDEN, YAN FUBIKU PC
 C12Q1/68, C12N15/00, G01N27/447, G01N27/447;
 CC strandedness, Single;
 topology: Linear;
 FH Key
 PH Location/Qualifiers
 FT source 1..27
 /organism="Artificial sequences" FT
 misc_feature 1..27
 /notes="Alu specific primer".
 FT Location/Qualifiers
 source 1..27
 /organism="unidentified" FT
 /mol_type="genomic DNA" FT
 /db_xref="taxon:32644"

ORIGIN

Query Match 67.0%; Score 13.4; DB 2; Length 27;
 Best Local Similarity 73.7%; Pred. No. 4.7e+04;
 Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTTACATCTCCAGTC 20
 Db 20 GAGCYRAGTCGAGGT C 2

RESULT 15

A24719/C A24719 28 bp DNA linear PAT 24-JAN-1995

LOCUS A24719 2065 .

DEFINITION Primer 2065.

ACCESSION A24719

VERSION A24719.1 GI:833452

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 28)

AUTHORS Little,S., Ferrie,R.M. and Robertson,N.H.

TITLE Detection method for nucleotide sequences

JOURNAL Patent: EP 0497527-A 05-AUG-1992;

IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED

FEATURES Location/Qualifiers

Source 1..28

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 65.0%; Score 13; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.8e+00;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACATCTCCAGT 19
 Db 27 AACATCTCCAGT 15

Search completed: May 21, 2006, 22:09:02
 Job time : 1032.5 secs

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OM nucleic - nucleic search, using sw model.

Run on: May 21, 2006, 21:34:08 ; Search time 386 Seconds
(without alignments)

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaggtaaacatctccaaatgc 20

Scoring table: IDENTITY_NUC

Gapext 1.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Genesegn_8:
 1: Genesegn1980s:
 2: Genesegn1990s:
 3: Genesegn2000s:
 4: Genesegn2001a:
 5: Genesegn2001b:
 6: Genesegn2002a:
 7: Genesegn2002b:
 8: Genesegn2003a:
 9: Genesegn2003b:
 10: Genesegn2003c:
 11: Genesegn2003d:
 12: Genesegn2004a:
 13: Genesegn2004b:
 14: Genesegn2005a:
 15: Genesegn2006s:
 ...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	20	100.0	20	13 ADQ88723	Adq88723 Human hyp
C 2	20	100.0	20	13 ADQ88724	Adq88724 Human HIF
C 3	20	100.0	49	8 ABZ76611	ABZ76611 Human HIF
C 4	15.6	80.0	16	10 AAL56916	AAL56916 Human hyp
C 5	15.2	76.0	21	14 AEA15801	AEA15801 Human Ent
C 6	14.2	71.0	26	14 ABC27934	ABC27934 Human all
C 7	14.2	71.0	26	14 ABC25568	AEC25568 Human all
C 8	14.2	71.0	30	12 ADQ31421	ADQ31421 Human CFT
C 9	14	70.0	49	8 ABZ76613	ABZ76613 Human HIF
C 10	13.8	69.0	25	9 ACT11456	ACT11456 Human mic
C 11	13.8	69.0	36	14 ABD66358	AED66358 Recombina
C 12	13.8	69.0	36	14 AED66354	AED66354 Recombina
C 13	13.8	69.0	41	6 ABZ23750	ABZ23750 Human mem
C 14	13.8	69.0	41	6 ABZ23750	ABZ23750 Human mem
C 15	13.6	68.0	27	12 ADQ31172	ADQ31172 Human ger
C 16	13.6	68.0	30	3 AA76302	AA76302 Mycobact
C 17	13.6	68.0	40	2 AAX24853	AAX24853 Primer J4
C 18	13.6	68.0	40	5 AAF30251	AAF30251 Dystrophi

ALIGNMENTS

RESULT 1	
ID	ADQ88723/C
XX	standard; DNA; 20 BP.
AC	ADQ88723;
XX	
DT	21-OCT-2004 (first entry)
XX	
DB	Human hypoxia inducible factor-1 gene fragment seqid 2.
XX	
KW	RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2004152655-A1.
XX	
PD	05-AUG-2004.
XX	
PF	28-JUN-2004; 2004US-00766185.
XX	
PR	31-JAN-2003; 2003US-0444367P.
XX	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	20	100.0	20	13 ADQ88723	Adq88723 Human hyp
C 2	20	100.0	20	13 ADQ88724	Adq88724 Human HIF
C 3	20	100.0	49	8 ABZ76611	ABZ76611 Human HIF
C 4	15.6	80.0	16	10 AAL56916	AAL56916 Human hyp
C 5	15.2	76.0	21	14 AEA15801	AEA15801 Human Ent
C 6	14.2	71.0	26	14 ABC27934	ABC27934 Human all
C 7	14.2	71.0	26	14 ABC25568	AEC25568 Human all
C 8	14.2	71.0	30	12 ADQ31421	ADQ31421 Human CFT
C 9	14	70.0	49	8 ABZ76613	ABZ76613 Human HIF
C 10	13.8	69.0	25	9 ACT11456	ACT11456 Human mic
C 11	13.8	69.0	36	14 ABD66358	AED66358 Recombina
C 12	13.8	69.0	36	14 AED66354	AED66354 Recombina
C 13	13.8	69.0	41	6 ABZ23750	ABZ23750 Human mem
C 14	13.8	69.0	41	6 ABZ23750	ABZ23750 Human mem
C 15	13.6	68.0	27	12 ADQ31172	ADQ31172 Human ger
C 16	13.6	68.0	30	3 AA76302	AA76302 Mycobact
C 17	13.6	68.0	40	2 AAX24853	AAX24853 Primer J4
C 18	13.6	68.0	40	5 AAF30251	AAF30251 Dystrophi

New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in several cancer cells.

Example 4; SEQ ID NO 3; 35pp; English.

The invention describes a compound, RX-0047 or RX-0149 targeted to a

nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), where the oligonucleotide compound inhibits the expression of human HIF-1. Also described are: a method of inhibiting the expression HIF-1 in human cells or tissues; and a method of inducing cytotoxicity in a cancer cell. Specifically claimed are RX-0047 and RX-0149 compounds having a fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5, aatggccaccgttccaa 3', and SEQ ID NO. 4, 5', ggagcttacatccaaatgc 3', respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The antisense compounds are also useful for preventing or delaying infection, inflammation, or tumour formation. This sequence represents a site on HIF-1 to which antisense oligonucleotides can be targeted in order to control HIF-1 gene expression.

Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCAAAGTC 20
Db 20 GGAGCTAACATCCAAAGTC 1

RESULT 2
ADQ88724

ID ADQ88724 Standard; DNA; 20 BP.

XX ADQ88724 ;

AC XX 21-OCT-2004 (first entry)

XX Human HIF-1 antisense oligonucleotide RX-0149.

XX RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity; cancer; infection; inflammation; tumour formation; ss; antisense Oligonucleotide; antisense technology.

XX Homo sapiens.

XX US2004152655-A1.

XX 05-AUG-2004 .

XX 28-JAN-2004; 2004US-00766185.

XX 31-JAN-2003; 2003US-0444367P.

XX (YOON /) YOON H.

PA (MAOL /) MAO L.

PA (LEEV /) LEE Y. B.

PA (AHNC /) AHN C.

PA (JIAN /) JIANG X.

XX PI Yoon H., Mao L., Lee YB., Ahn C., Jiang X;

XX DR WPI; 2004-148670/14.

XX New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), useful for inhibiting expression of HIF-1 and inducing cytotoxicity in several cancer cells.

XX Claim 6; SEQ ID NO 4; 35pp; English.

XX The invention describes a compound, RX-0047 or RX-0149 targeted to a nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), where the oligonucleotide compound inhibits the expression of human HIF-1. Also described are: a method of inhibiting the expression HIF-1 in human cells or tissues; and a method of inducing cytotoxicity in a cancer cell. Specifically claimed are RX-0047 and RX-0149 compounds having a fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5,

CC aatggccaccgttccaa 3', and SEQ ID NO. 4, 5', ggagcttacatccaaatgc 3', respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The antisense compounds are also useful for preventing or delaying infection, inflammation, or tumour formation. This sequence represents a human HIF-1 antisense oligonucleotide.

XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCAAAGTC 20
Db 1 GGAGCTAACATCCAAAGTC 20

RESULT 3
ABZ76611

ID ABZ76611 standard; DNA; 49 BP.

XX AC ABZ76611 ;

XX 30-APR-2003 (first entry)

XX Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.

XX DE ID ABZ76611

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;

XX KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;

XX KW tumor; nuclear localisation signal; oxygen dependent degradation domain; NLS;

XX ODD; PCR primer; oxygen dependent degradation domain;

XX Homo sapiens.

XX OS WO200299104-A1.

XX PN 04-JUN-2002; 2002WO-JP0003482.

XX PR 05-JUN-2001; 2001JP-00165948.

XX PR 05-JUN-2001; 2001JP-00165949.

XX PA (POK) POLA CHEM IND INC.

XX PA (HIRAOKA M. /) HIRAOKA M.

XX PA (KOND OH S. /) KOND OH S.

XX PI Hiraoka M., Kondoh S., Harada H;

XX DR WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX PS Example; Page 24; 14pp; Japanese.

XX The present invention describes DNA encoding hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDPMLAP1PMDDFQL see ABP5769) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA, (2) cells transformed by the vectors, (3) producing the fusion protein by culture of the transformed cells, (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA, (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein, (7) fusion proteins encoded by the DNA, and (8) stabilisation of proteins under specific conditions of oxygen tension. (1) has cyostatic activity, and can be used for the

CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (I) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention

XX Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
Db 26 GGAGCTAACATCTCCAGTC 45

RESULT 4
AAU56916 standard; DNA; 16 BP.
ID AAU56916;
XX AC
XX DT 11-MAR-2004 (first entry)
DB Human hypoxia-inducible factor-1 alpha antisense oligo #12.

KW HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer; pre-eclampsia; cyrostatic; gynaecological; antiinflammatory; nootropic; neuroprotective; ss.

XX OS Homo sapiens.

XX PN WO2003085110-A2.

XX PD 16-OCT-2003.

XX PP 04-APR-2003; 2003WO-1B001758.

XX PR 05-APR-2002; 2002US-0370126P.

XX (CURE-) CURBON AS.

XX PA Thruv CA, Hog AM, Kristjansen PEG;

XX DR 2003-812728/76.

XX New oligonucleotide that modulates hypoxia-inducible factor-1alpha, useful for treating e.g. cancer or Alzheimer's disease.

Claim 1; Page 41; Opp; English.

XX The present invention relates to compounds capable of modulating hypoxia-inducible factor-1alpha (HIF1α). The compounds are used to treat patients with, or at risk of developing, cancer (e.g. of breast, prostate, pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's disease, for modulating angiogenesis, proliferation of erythrocytes and other cells, iron, glucose and energy metabolism, pH regulation tissue invasion, apoptosis, multiple drug resistance, cellular stress responses, and matrix metabolism, especially apoptosis where modulation is sensitive to an apoptotic stimulus, particularly a chemotherapeutic agent and for inhibiting proliferation of cells (especially cancer cells) in vitro. The present sequence is an antisense oligonucleotide against HIF1alpha identified in the exemplification of the invention

XX Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Mismatches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCAGTC 19

Db 1 GCTAACATCTCCAGTC 16
XX RESULT 5
ID AEA15801 standard; DNA; 21 BP.
XX AC AEA15801;
XX DT 28-JUL-2005 (first entry)
DB Human Enterobacterium detection-related PCR primer SeqID33.
XX KW microorganism detection; microorganism identification; DNA detection; DNA amplification; enterobacteriaceae infection; antibiotic; PCR; primer; ss.
XX OS Bacteria.
XX PN JP2005124495-A.
XX PD 19-MAY-2005.
XX PP 24-OCT-2003; 2003JP-00364188.
XX PR 24-OCT-2003; 2003JP-00364188.
XX PA (HONS) YAKULT HONSHA KK.
XX DR WPI; 2005-359465/37.
XX Novel Primer comprising specific nucleotide sequences, useful for PT detection and identification of human Enterobacterium such as Clostridium butyricum.
XX Claim 1; SEQ ID NO 33; 20pp; Japanese.
CC This invention relates to a novel PCR primer for detecting human Enterobacterium, comprising one of 39 fully defined 18-26 nucleotide sequences (SEQ ID No. 1-39) given in the specification or a sequence complementary to the above mentioned base sequence. The invention enables rapid and convenient detection and identification of human Enterobacterium. The present sequence is that of a PCR primer which was used for detecting human Enterobacterium in the method of the invention.
XX PS Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
CC This invention relates to a novel PCR primer for detecting human Enterobacterium, comprising one of 39 fully defined 18-26 nucleotide sequences (SEQ ID No. 1-39) given in the specification or a sequence complementary to the above mentioned base sequence. The invention enables rapid and convenient detection and identification of human Enterobacterium. The present sequence is that of a PCR primer which was used for detecting human Enterobacterium in the method of the invention.
XX SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX Query Match 76.0%; Score 15.2%; DB 14; Length 21;
CC Best Local Similarity 85.0%; Pred. No. 8.2e+02;
CC Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC RESULT 6
ID AEC27934 standard; DNA; 26 BP.
XX AC AEC27934;
XX DR 17-Nov-2005 (first entry)
DB Human allele-specific oligonucleotide #3954.
XX KW Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP; major histocompatibility complex; MHC; HLA; human leukocyte antigen; immune disorder; inflammation; inflammatory bowel disease;
KW ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes; diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;
KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;

rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;

dermatomyositis; pernicious anemia; primary biliary cirrhosis;

idiopathic thrombocytopenia purpura; Sjögren's syndrome;

multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;

gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive;

arthrarthritic; antirheumatic; antidiabetic; muscular-gen.;

neuroprotective; dermatological; antithyroid; hepatotropic; antiangiemic;

hemostatic; ophthalmological; uropathic; antipsoriatic; ss;

SNP detection.

XX Homo sapiens.

XX WO20050502110-A2.

PN 09-SEP-2005.

PD 28-FEB-2005; 2005WO-US006628.

PR 26-FEB-2004; 2004US-0547823P.

XX 26-FEB-2004; 2004US-0547823P.

PR XX PA (ILLU-) ILLUMINA INC.

PA XX XX

XX PT Oliphant A, Murray S;

XX DR XX

XX WPI; 2005-638856/65.

XX PT Identifying single nucleotide polymorphism (SNP) haplotype that

PT correlates with the HLA type, useful for diagnosing an immunological or

PT inflammatory condition, comprises providing SNPs in the major

PT histocompatibility complex region.

XX PS Example 1; SEQ ID NO 3954; 175PP; English.

XX XX

CC The invention relates to a method of identifying the nucleotide for each

CC of a set of single nucleotide polymorphisms (SNPs) in the major

CC histocompatibility complex (MHC) region in a population of individuals,

CC comprising providing the HLA type for the individuals and identifying an

CC SNP haplotype in the population that correlates with the HLA type, where

CC the SNP haplotype comprises the SNPs in the MHC region. The invention

CC also relates to a method of predicting the HLA type of an individual, a

CC method of determining the presence or absence of an allelic variant of an

CC MHC gene in an individual, a method of identifying an SNP haplotype that

CC correlates with susceptibility of an individual to a disease or

CC condition. The disease or condition is an immune disorder or inflammatory

CC condition selected from inflammatory bowel disease, ulcerative colitis,

CC Crohn's disease, rheumatoid arthritis, diabetes mellitus,

CC myasthenia gravis, vitiligo, Graves' disease, Hashimoto's disease,

CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic

CC lupus erythematosus, polymyositis, dermatomyositis, pernicious anemia, Sjögren's syndrome, multiple sclerosis, idiopathic thrombocytopenia

CC purpura, psoriasis. This sequence represents a human allele-specific

CC oligonucleotide used in the scope of the invention.

XX Sequence 26 BP; 5 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

SQ Query Match 71.0%; Score 14.2; DB 14; Length 26;

Best Local Similarity 84.2%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 3;

Indels 0; Gaps 0; Gaps 0;

XX QY 2 GAGCTAACATCTCCAAGTC 20

DB 5 GACCTAACATCTCCAATCTC 23

SQ Sequence 26 BP; 6 A; 7 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 26;

Best Local Similarity 84.2%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 3;

Indels 0; Gaps 0; Gaps 0;

XX QY 2 GAGCTAACATCTCCAAGTC 20

DB 5 GACCTAACATCTCCAATCTC 23

SQ Sequence 26 BP; 6 A; 7 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 26;

Best Local Similarity 84.2%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 3;

Indels 0; Gaps 0; Gaps 0;

XX QY 2 GAGCTAACATCTCCAAGTC 20

DB 5 GACCTAACATCTCCAATCTC 23

SQ Sequence 26 BP; 6 A; 7 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 14; Length 26;

Best Local Similarity 84.2%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 3;

Indels 0; Gaps 0; Gaps 0;

XX QY 2 GAGCTAACATCTCCAAGTC 20

DB 5 GACCTAACATCTCCAATCTC 23

RESULT 8

AD031421 AD031421 standard; DNA; 30 BP.

XX AD031421;

XX DT 26-AUG-2004 (first entry)

DE Human CFTR gene mutant probe for variant 1717-1G>A #2.

KW Human; CFTR gene; SS; probe; cystic fibrosis;

KW Cystic fibrosis Transmembrane Conductance Regulator;

KW invasive cleavage structure assay; INVADER; PREP;

KW fluorescent resonance energy transfer; multiplexed amplification.

OS Homo sapiens.

PN WO2004046688-A2.

XX PD 03-JUN-2004.

XX PP 14-NOV-2003; 2003WO-US036611.

XX PR 14-NOV-2002; 2002US-0426144P.

PR 21-FEB-2003; 2003US-00371913.

PR 26-JUN-2003; 2003US-00606577.

PR 21-JUL-2003; 2003US-0489095P.

PR 25-AUG-2003; 2003US-049764D.

PR 28-OCT-2003; 2003US-0515175P.

PR 14-NOV-2003; 2003US-00713653.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Accola M, Wigdal SS, Mast AL, Bartholomay CT, Kwiatkowski RW;

PI Tevere V, IP HS, Carroll K, Peterson P, Agarwal P, Jarvis N;

PI Hall JG, Heisler L;

XX DR 2004-420702/39.

XX PS Example 7; SEQ ID NO 52; 147pp; English.

XX The invention relates to detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) alleles comprising providing a sample comprising a CFTR target nucleic acid, amplifying the CFTR target nucleic acid with 25 cycles or fewer of a PCR to generate amplified target nucleic acid, and exposing the amplified target nucleic acid to detection assays configured to detect CFTR alleles under conditions such that the presence or absence of the CFTR alleles is detected, using an invasive cleavage structure assay (designated INVADER), employing FRET probes (fluorescent resonance energy transfer). Also included is a kit comprising a non-amplified oligonucleotide detection assay configured for detecting at least one CFTR allele or oligonucleotide detection assays configured for detecting a set of CFTR alleles where the set is a first set comprising 2789+5G to A, R1162X, 189+1 G to A, del1507, N1303K, and A455E, a second set comprising 3120-1G to A, 3659delC, G551D, N1078delT, R334W, 711+1G to T, and 3849-10kb, a third set comprising 621+1G to T, R282X, 1717-1G to A, and R117H, or a fourth set comprising R347P, G85E, G342X and R553X, or a fifth set comprising 2184delA. The non-amplified oligonucleotide detection assay or the oligonucleotides configured to form an invasive cleavage structure in combination with target sequence comprising the CFTR allele. The first oligonucleotide comprises a 5' portion and a 3' portion, where the 3' portion is configured to hybridise to the target sequence and the 5' portion is configured to not hybridise to the target sequence. The second oligonucleotide comprises a 5' portion and a 3' portion, where the 5'

CC portion is configured to hybridise to the target sequence and the 3' CC portion is configured to not hybridise to the target sequence. The method CC and kit are useful for detecting CFTR alleles, more particularly for screening nucleic acid samples e.g. from patients, for the presence of any one of a collection of mutations in the CFTR gene associated with cystic fibrosis. The method and compositions are useful for generating and analysing limited cycle, multiplexed amplification of a large collection of CFTR loci. The present sequence comprises a probe for the method of the invention detecting the mutant CFTR allele.

XX SQ Sequence 30 BP; 9 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2%; DB 12; Length 30;

Best Local Similarity 84.2%; Prod. No. 2.8e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGT 19

Db 9 GGAGAGACATCTCCAAGT 27

XX RESULT 9 ABZ76613

ID ABZ76613 standard; DNA; 49 BP.

XX AC ABZ76613;

XX DT 30-APR-2003 (first entry)

XX Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:26.

XX DB Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:26.

XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic; hypoxic; solid tumour; gene therapy; microbial fermentation; medicine; tumour; nuclear localisation signal; oxygen dependent degradation domain;

XX KW NLS; ODD; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200399104-A1.

XX DR 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POK) POLA CHEM IND INC.

PA (HIRAKA) HIRAKA M.

PA (KOND) KOND OH S.

XX PI Hirakawa M, Kondoh S, Harada H;

XX DR WPI; 2003-148670/14.

XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX PS Example 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLBMMLAPITMMDBPQL see ABP5769) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic

conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (I) has cytostatic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (I) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIP-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention.

```

2 Sequence 49 BP; 15 A; 10 C; 11 G; 13 T; 0 U; 0 Other;
Query Match 70.0%; Score 14; DB: 8; Length: 49;
Best Local Similarity 100.0%; Pred. No. 3.8e+3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; GC
1 GGAGCTTAACATCTC 14
| | | | | | | | | | |
35 GGAGCTTAACATCTC 48

```

RESULT 10
ACI11456/C Human microarray DNA oligonucleotide SEQ ID NO 11447.
ACI11456 standard; DNA; 25 BP.
ACI11456;
13-OCT-2003 (first entry)
EST, 88; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
Homo sapiens.
US2003104410-A1.
05-JUN-2003.
15-MAR-2002; 2002US-00098263.
16-MAR-2001; 2001US-0276759P.
(AFFY-) AFFYMATRIX INC.

Mittmann MP;
WPI: 2003-567953/53.
New array of nucleic acid probes, useful for in situ hybridization, including Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1, SEQ ID NO 11447; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in *in situ* hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific

mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdb.uspto.gov/seQUENCE.html

RESULT 11
AED66358
ID AED66358 standard; DNA; 36 BP.

AC	AED63358;
XX	
DT	29-DEC-2005 (first entry)
XX	
DE	Recombinant cytochrome P450 related P4503A4-Hsp70 sequence N.
XX	
KW	expression; cytochrome P450; heat shock protein; protein synthesis; protein folding; Gene expression; Hsp70; ds.
XX	
OS	Unidentified.
XX	

KR2005028279-A.
PN
AA

PD 22-MAR-2005.
XX

1A-SEP-2003: 20003KB-00065447
PP

X (AHNT/) AHN T H.
P

PI Ahn TH, Yang SY,
KK

XX Method for determining essential communication and concluding sentence of

recombinant cytochrome p450 enzymes by co-expression with genes encoding heat shock proteins which function as molecular chaperone.

PS Disclosure; Page 3; 8pp; Korean.
XX

The invention relates to a method for increasing plant growth by catalytic activity of recombinant cytochrome P450 enzymes by co-

shock proteins function as a molecular chaperone that regulate other protein synthesis and translocation, protein folding, gene expression,

CC proteins induce increased protein expression and catalytic activity of
CC recombinant cytochrome P450 enzymes. The method for increasing protein

CC expression and catalytic activity of recombinant cytochrome P450 enzymes comprises co-expression of the recombinant cytochrome P450 enzyme genes

CC recombinant cytochrome P450 enzyme genes and the heat shock protein genes CC are isolated from human or rat; the recombinant cytochrome P450 enzyme CC

Genes and the heat shock protein genes are contained in one open reading frame, and the heat shock proteins induce increased amount and catalytic

CC represents DNA relating to the present invention.
XX

卷之三

Query Match, Similarity 69.0%; Score 13.8; DB 14; Length 36;
 Best Local Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
 AB223749 standard; DNA; 41 BP.
 ID AB223749
 XX
 AC
 XX
 DT 26-MAR-2003 (first entry)
 XX
 DE Human membrane vacuole transportation related protein 10.23 probe 1.
 XX
 KW Human; membrane vacuole transportation protein; HIV; 10.23; malignant tumour;
 KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
 KW inflammation; probe; 88.
 XX
 OS Homo sapiens.
 XX
 PN CN1345930-A.
 XX
 PD 24-APR-2002.
 XX
 PP 29-SEP-2000; 2000CN-00125514.
 XX
 PR 29-SEP-2000; 2000CN-00125514.
 XX
 PA (SHAN-) SHANGHAI BIOMINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR 2002-584316/63.
 XX
 PT A novel human membrane vacuole transportation related protein 10.23
 PT polypeptide, useful for curing several diseases e.g. malignant tumor,
 PT hemopathy, HIV infection, immunological disease and various inflammations
 PT and epilepsy.
 XX
 PS Example 6; Page 19 (disclosure); 33pp; Chinese.
 XX
 CC The invention relates to a human membrane vacuole transportation related
 CC protein 10.23. Also disclosed are the polynucleotide encoding the
 CC polypeptide, and a method for preparing the polypeptide using DNA
 CC recombination techniques. The polypeptide is useful for curing several
 CC diseases including, malignant tumors, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological disease and various inflammations.
 CC The current sequence represents a human membrane vacuole transportation
 CC related protein 10.23 related probe sequence
 XX
 SQ Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;
 Query Match 69.0%; Score 13.8; DB 6; Length 41;
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GCTAACATCTCCAAGTC 20
 | | | | | | | | | | | |
 Db 23 GGTAACAGCTCCAAAGTC 39

RESULT 14
 AB223750 standard; DNA; 41 BP.
 ID AB223750
 XX
 DE Human membrane vacuole transportation related protein 10.23 probe 2.
 XX
 KW Human; membrane vacuole transportation protein; HIV; 10.23; malignant tumour;
 KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
 KW inflammation; probe; 88.
 XX
 OS Homo sapiens.

Query Match, Similarity 69.0%; Score 13.8; DB 14; Length 36;
 Best Local Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
 AED66354 standard; DNA; 36 BP.
 ID AED66354;
 XX
 DT 29-DEC-2005 (first entry)
 XX
 DB Recombinant cytochrome P450 related P4501A2-Hsp70 sequence N.
 XX
 KW expression; cytochrome P450; heat shock protein; protein synthesis;
 KW protein folding; gene expression; Hsp70; ds.
 XX
 OS Unidentified.
 XX
 PN KR2005028279-A.
 XX
 PD 22-MAR-2005.
 XX
 PP 18-SEP-2003; 2003KR-00065447.
 XX
 PR 18-SEP-2003; 2003KR-00065447.
 XX
 PA (AHNT/) AHN T H.
 XX
 PI Ahn TH, Yang SY;
 XX
 DR 2005-579519/59.
 XX
 PT Method for increasing protein expression and catalytic activity of
 PT recombinant cytochrome p450 enzymes by co-expression with genes encoding
 PT heat shock proteins which function as molecular chaperone.
 XX
 PS Disclosure; Page 2; 8pp; Korean.
 XX
 The invention relates to a method for increasing protein expression and
 catalytic activity of recombinant cytochrome P450 enzymes by co-
 expression with genes encoding heat shock proteins (HSPs), where the heat
 shock proteins function as a molecular chaperone that regulate other
 protein synthesis and translation, protein folding, gene expression,
 protein hydrolysis, protein aggregation, etc., so that the heat shock
 proteins induce increased protein expression and catalytic activity of
 recombinant cytochrome P450 enzymes. The method for increasing protein
 expression and catalytic activity of recombinant cytochrome P450 enzymes
 comprises co-expression of the recombinant cytochrome P450 enzymes
 with genes encoding heat shock proteins Hsp70 and HDJ-1, wherein the
 recombinant cytochrome P450 enzyme genes and the heat shock protein genes
 are isolated from human or rat; the recombinant cytochrome P450 enzyme
 genes and the heat shock protein genes are contained in one open reading
 frame, and the heat shock proteins induce increased amount and catalytic
 activity of the recombinant cytochrome P450 enzymes. This sequence
 represents DNA relating to the present invention.
 XX
 Sequence 36 BP; 11 A; 11 C; 10 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 69.0%; Score 13.8; DB 14; Length 36;
 Best Local Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
 AB223750 standard; DNA; 41 BP.
 ID AB223750
 XX
 DE Human membrane vacuole transportation related protein 10.23 probe 2.
 XX
 KW Human; membrane vacuole transportation protein; HIV; 10.23; malignant tumour;
 KW haemopathy; human immunodeficiency virus; HIV; immunological disease;
 KW inflammation; probe; 88.
 XX
 OS Homo sapiens.

XX CN1345830-A.
 XX PD 24-APR-2002.
 XX PP 29-SEP-2000; 2000CN-00125514.
 XX PR 29-SEP-2000; 2000CN-00125514.
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX PI Mao Y, Xie Y;
 XX DR WPI; 2002-584316/63.
 XX SQ Sequence 27 BP; 6 A; 4 C; 8 G; 9 T; 0 U; 0 Other;

PT protein (GANP) gene for production of high-affinity antibodies as diagnostic reagents and disease therapy.

XX PS Example 10; SEQ ID NO 30; 214BP; Japanese.

CC The invention relates to transgenic non-human animals and their offspring which are transformed with germinal center associated nuclear protein (GANP) gene. The GANP gene, encoded protein and transgenic animals express GANP can be used for the production of high-affinity antibodies to viral antigens for treatment and prevention of infection by viruses such as human immunodeficiency virus and hepatitis C virus. This sequence corresponds to a PCR primer to amplify a the human GANP gene.

XX Sequence 27 BP; 6 A; 4 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6%; DB 12; Length 27;
 Best Local Similarity 80.0%; Pred. No. 5.6e+3;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Caps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
 Db 23 GGTGAAACATCTCAAGTC 4

Search completed: May 21, 2006, 22:31:22
 Job time : 390 secs

CC A novel human membrane vacuole transportation related protein 10.23 polypeptide, useful for curing several diseases e.g. malignant tumor, hemopathy, HIV infection, immunological disease and various inflammations and epilepsy.

CC Example 6; Page 19 (disclosure); 33pp; Chinese.

CC The invention relates to a human membrane vacuole transportation related protein 10.23. Also disclosed are the polynucleotide encoding the polypeptide, and a method for preparing the polypeptide using DNA recombination techniques. The polypeptide is useful for curing several diseases including, malignant tumours, haemopathy, human immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The current sequence represents a human membrane vacuole transportation related protein 10.23 related probe sequence

XX SQ Sequence 41 BP; 9 A; 15 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8%; DB 6; Length 41;
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCAGTC 20
 Db 23 GCTAACAGCTCCAGTC 39

RESULT 15
 ADO31172/C
 ID ADO31172 standard; DNA; 27 BP.
 XX AC ADO31172;
 XX DT 12-AUG-2004 (first entry)
 DIS Human Germinal center associated nuclear protein gene primer #26.
 XX KW primer; virucide; viral antigen inhibitor; transgenic;
 KW germinal center associated nuclear protein; GANP; antibody;
 KW virus infection; human immunodeficiency virus; hepatitis C virus.
 OS Homo sapiens.
 XX PN WO2004040971-A1.
 XX PD 21-MAY-2004.
 XX PP 07-NOV-2003; 2003WO-JP014221.
 XX PR 07-NOV-2002; 2002WO-JP011598.
 XX PA (IMMU-) IMMUNOKICK INC.
 XX PI Sakaguchi N;
 XX DR WPI; 2004-411378/38.
 XX PT Transgenic mammal transformed with germinal center associated nuclear

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OM nucleic - nucleic search, using sw model.

Run on: May 21, 2006, 21:49:17 ; Search time 2196 Seconds
(without alignment)
509.284 Million cell updates/sec

Title: US-10-766-185-4

Pefect score: 20

Sequence: 1 ggagcttaacatctccaaatcggc 20

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
 1: gb_est1;*
 2: gb_est3;*
 3: gb_est4;*
 4: gb_est1;*
 5: gb_est5;*
 6: gb_htc;*
 7: gb_est2;*
 8: gb_est3;*
 9: gb_est0;*
 10: gb_est9;*
 11: gb_g961;*
 12: gb_g962;*
 13: gb_g963;*
 14: gb_g964;*

EST:
 1: gb_est1;*
 2: gb_est3;*
 3: gb_est4;*
 4: gb_est1;*
 5: gb_est5;*
 6: gb_htc;*
 7: gb_est2;*
 8: gb_est3;*
 9: gb_est0;*
 10: gb_est9;*
 11: gb_g961;*
 12: gb_g962;*
 13: gb_g963;*
 14: gb_g964;*

gb_g964;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	14.4	AZ352012	26	11	AZ352012 1M0090M13
c	2	14.2	72.0	11	AZ352012 2M0165J04
c	3	13.8	71.0	49	A1348359
c	4	13.4	69.0	49	A1348359
c	5	13.2	67.0	50	A1348359
c	6	13.2	66.0	47	A1348359
c	7	13.2	66.0	47	A1348359
c	8	13.2	66.0	49	A1348359
c	9	12.8	64.0	50	A1348359
c	10	12.8	64.0	32	A1348359
c	11	12.6	63.0	41	A1348359
c	12	12.4	63.0	28	A1348359
c	13	12.2	62.0	34	A1348359
c	14	12.2	61.0	28	A1348359
c	15	12.2	61.0	35	A1348359
c	16	12.2	61.0	37	A1348359
c	17	12.2	61.0	46	A1348359
c	18	12	60.0	8	A1348359
c	19	12	60.0	33	A1348359

ALIGNMENTS

RESULT 1
AZ352012

LOCUS 1M0090M13P Mouse 1.0kb plasmid UGCGC1 library GSS 29-SEP-2000 DEFINITION clone UGCGC1M0090M13 F, genomic survey sequence.

ACCESSION AZ352012

VERSION AZ352012.1 GI:10431249

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

DEFINITION Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridoidea; Muridae; Murinae; Mus.

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beaumont, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: odunngene@utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0090 row: M column: 13

Seq Primer: CGTGTAAAAGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 26.

Location Qualifiers 1..26

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/mo_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGC1M0090M13"
/sex="Male"

AG191947 Pan trogl.
AM111394 AM111394
AZ785517 2M029M22
AA308443 OR81a03-B
AA308443
AZ473316 1M028HG07
AZ806107 2M0067N24
AU258458 AU258458
AU258458
AZ7776209 2M0009J120
BX289673 Arabidops
BH909732 Arabidops
AH771809 Arabidops
BX535253 Arabidops
A2321341 1M0041B20
AZ797513 2M0053H15
AZ450961 1M0450B05
BX289417 Arabidops
DX060578 KB-FB066N1
R60473 Yh13906_r1
CC798230 SALK 1460
A2806105 2M0067N24
A2592491 1M0403019
CG715229 1119040B1
AG199568 Pan trogl.
BH405909 RPCI-23-1
BH904515 SALK 1046
AA276118 vc36d18

FEATURES Source

Result No.	Score	Query	Match Length	DB ID	Description
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c	3	13.8	71.0	49	A1348359
c	4	13.4	69.0	49	A1348359
c	5	13.2	67.0	50	A1348359
c	6	13.2	66.0	47	A1348359
c	7	13.2	66.0	49	A1348359
c	8	13.2	66.0	50	A1348359
c	9	12.8	64.0	32	A1348359
c	10	12.8	64.0	41	A1348359
c	11	12.6	63.0	28	A1348359
c	12	12.4	62.0	34	A1348359
c	13	12.2	61.0	28	A1348359
c	14	12.2	61.0	35	A1348359
c	15	12.2	61.0	37	A1348359
c	16	12.2	61.0	46	A1348359
c	17	12.2	61.0	48	A1348359
c	18	12	60.0	33	A1348359
c	19	12	60.0	34	A1348359

/lab хозяин="E. Coli strain XL10-Gold, T₁-resistant, F-"
 /clone имя="Mouse Plasmid library"
 /note "Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male)" was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.Jax.org/resources/documents/dnare/>). The DNA
 was hydrodynamically sheared by repeated passage through
 a 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (9114732114 [gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed
 to adaptors complementary to the vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance.

ALIGN	Query Match	Score 14.4;	DB 11;	Length 26;	
/	Best Local Similarity 93.8%; Matches 15;	Pred. No. 1.8e+04; Conservative 0;	Mismatches 1;	Indels 0;	Gaps
2	GAGCTAACATCTCCA 17				
2	GAGCTCACATCTCCA 17				

RESULT 2	
AZ860255	C
CCUS	47 bp
DEFINITION	DNA linear
2M016J04F Mouse 10kb plasmid UGCGCM library Mus musculus genomic clone UGCGCM016J04 F, genomic survey sequence.	GSS 21-FEB-2001
ACCESSION	AZ860255
A2861255	AZ860255.1
GI:13055225	
GSS.	
KEYWORDS	
Mus musculus (house mouse)	
ORGANISM	
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
Sciuromorpha; Murioidea; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 47)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingay, A., von Niederhäusern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10 kb plasmid inserts

JOURNAL
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Errror: 0.00
 Plate: 0166 row: J column: 04
 Seg primer: CGTTGTAACGAGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 47.
 Location/Qualifiers
 1. .47
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CS7BL/6J"
 /db_xref="Taxon:10090"
 /clade="mammal"

Sex: "Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PW424iv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnarecs/>). The DNA
was hydrodynamically sheared by repeated passage through
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA Polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD18 (Giga 4732114 Gb AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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    71.0%; Score 14.2; DB 11;
  Identity 84.2%; Pred. No. 2.2e+04;
Conservative 0; Mismatches 3; Indels 0;
Gaps 0
ACATCTCCAAAGTC 20
GCAATTCCTTCAACTC 28

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K1 NCI CGAP Lus 49 bp mRNA linear EST 01-FEB-1999
 SW:RNA_HUMAN Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA
 R. ; mRNA sequence.
 1 GI:4085565
 ens (human)
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homo.
 1 to 49
<http://www.ncbi.nlm.nih.gov/ncicgap>
 Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Index (1997)

Robert Strausberg, Ph.D.
naps@MAIL.nih.Gov
Procurement: Christopher Moskaliuk, M.D., Ph.D., Michael R.
ick, M.D., Ph.D.
Library Preparation: M. Bento Soares, Ph.D.
Array by: Greg Lennon, Ph.D.
Sequencing by: Washington University Genome Sequencing Center
Distribution: NCI-CGAP clone distribution information can be
through the J.M.A.G.B. Consortium/LINL at:
linl.gov/bbtp/image/image.html

Considered overall poor quality

Length: 696 Std Error: 0.00
Quality sequence stop: 1.
Location/Qualifiers

1. .49

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/mol_type="mRNA"
/db_xref=taxon:9606"
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/tissue_type="carcinoïd"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ju5"
 /notes="Organ: lung; Vector: pT7T3D-PacI; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer.
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match	69.0%	Score 13.8;	DB 1;	Length 49;
Best Local Similarity	88.2%	Pred. No.	3.6e+04;	
Matches	15;	Mismatches	2;	Indels 0;
				Gaps 0;

Qy 1 GGAGCTAACATTCCAA 17
 Db 38 GTAGCTAACATTCCAA 22

RESULT 4
 CA795439/C
 LOCUS CA795439 50 bp mRNA linear EST 05-DEC-2002
 DEFINITION Theobroma cacao BL (Bean and Leaf from Amelonado type Cacao)
 Theobroma cacao CDNA clone Cac_BL_2476 5', mRNA sequence.
 CA795439
 VERSION EST
 CA795439.1 GI:26052215
 SOURCE Theobroma cacao (cacao)
 ORGANISM Theobroma cacao
 Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 Spermatophytina; Magnoliophytina; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma
 (bases 1 to 50)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
 Retzel, B.R. and Jones, C.A.
 Title L.) varieties
 L.) variety and microarray analysis of cacao (Theobroma cacao
 Planta 216 (2), 255-264 (2002)
 Contact: Jones, Paul
 Masterfoods
 3 Dunbee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.effem.com
 Seq Primar: T3.

FEATURES

source	Location/Qualifiers
1..50	Contact: Jones, Paul
/organism="Theobroma cacao"	
/mol_type="mRNA"	
/strain="Amelonado type"	
/db_xref="Taxon:3641"	
/clones="Cac_BL_2476"	
/tissue_type="Nature leaf and mature bean"	
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/dev_stage="maturity"	
/lab_host="XL-1 Blue MRF"	
/clone_lib="Cac_BL (Bean and Leaf from Amelonado type Cacao)"	
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."	

ORIGIN

Query Match	67.0%	Score 13.2;	DB 4;	Length 50;
Best Local Similarity	93.3%	Pred. No.	5.8e+04;	
Matches	14;	Mismatches	1;	Indels 0;
				Gaps 0;

Qy 2 GAGCTAACATTCCAA 16
 Db 43 GAGCTAACATTCCAA 29

Query Match 66.0% Score 13.2; DB 11; Length 47;
 Best Local Similarity 83.3%; pred. No. 7.3e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 AGCTAACATTCCAA 20

RESULTS 5

LOCUS AZ362217	47 bp DNA linear	GSS 02-OCT-2000
DEFINITION 1M0107B16P Mouse 10kb plasmid UGCGM library Mus musculus genomic sequence.		
ACCESSION A2362217		
VERSION AZ362217.1 GI:1047917		
KEYWORDS GSS.		
SOURCE Mus musculus (house mouse)		
ORGANISM Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE 1 (bases 1 to 47)		
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meinen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.		
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL Unpublished (2000)		
COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@gene.utah.edu Insert Length: 10000 Std Error: 0.00 Place: 0107 Row: B Column: 16 Seq primer: CGTTGTAACAGGGCCAGT Class: plasmid ends High quality sequence stop: 47.		
FEATURES source	Location/Qualifiers	
1..47	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-	
/clone_id="Mouse 10kb plasmid UGCGM library"	/note="Vector: PWD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/resource/documents/dnases/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF122072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
ORIGIN		

		FEATURES	source	
Db	18 AGATACATTACAAGTC 35			TDNA. This sequence lies within an annotated exon of At3g22540. Class: TDNA tagged.
RESULT 6				Location/Qualifiers 1. 49
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DEFINITION	Sub scrofa genomic clone PigE-48B8, genomic survey sequence.			/ecotype="Col-0"
ACCESSION	CT391862			/db_xref="taxon:3702"
VERSION	CT391862.1			/clone_id="SALK_152070.41.70.X"
KEYWORDS	Sus scrofa (pig)			/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html "
ORGANISM	Sus scrofa			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus				
REFERENCE	1. (bases 1 to 47)			
AUTHORS	Humphray,S.J., Plumb,R.W. and Durham,J.L.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk. Unpublished			
COMMENT	This sequence was generated from the SP6 end of BAC 48B8. 48B8 is part of the PigEBAC BAC Library created by Roslin Institute/RFGR. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/ .			
FEATURES				
SOURCE				
RESULT 7				
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DEFINITION	Sub scrofa genomic clone PigE-48B8, genomic survey sequence.			
ACCESSION	CT391862.1			
KEYWORDS	Sus scrofa (pig)			
ORGANISM	Sus scrofa			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus				
REFERENCE	1. (bases 1 to 47)			
AUTHORS	Humphray,S.J., Plumb,R.W. and Durham,J.L.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk. Unpublished			
COMMENT	This sequence was generated from the SP6 end of BAC 48B8. 48B8 is part of the PigEBAC BAC Library created by Roslin Institute/RFGR. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/ .			
FEATURES				
SOURCE				
RESULT 8				
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DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	AZ774523			
KEYWORDS	GSS.			
ORGANISM	Mus musculus (house mouse)			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 50)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Maenzen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah			
FEATURES				
SOURCE				
RESULT 9				
LOCUS	CC888587	LOCUS		
DEFINITION	49 bp DNA linear GSS 31-JUL-2003			
ACCESSION	CC888587			
KEYWORDS	CC888587.1			
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MATERIALS	Arabidopsis thaliana; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eu-rosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 10				
LOCUS	CATCTAACATCTCAAGTC 19	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 11				
LOCUS	CATCTAACATCTCAAGTC 21	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 12				
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DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 13				
LOCUS	CATCTAACATCTCAAGTC 25	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 14				
LOCUS	CATCTAACATCTCAAGTC 27	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 15				
LOCUS	CATCTAACATCTCAAGTC 29	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
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LOCUS	CATCTAACATCTCAAGTC 31	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
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LOCUS	CATCTAACATCTCAAGTC 33	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 18				
LOCUS	CATCTAACATCTCAAGTC 35	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 19				
LOCUS	CATCTAACATCTCAAGTC 37	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 20				
LOCUS	CATCTAACATCTCAAGTC 39	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 21				
LOCUS	CATCTAACATCTCAAGTC 41	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 22				
LOCUS	CATCTAACATCTCAAGTC 43	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				
RESULT 23				
LOCUS	CATCTAACATCTCAAGTC 45	LOCUS		
DEFINITION	50 bp DNA linear GSS 16-FEB-2001			
ACCESSION	CC888587			
KEYWORDS	CATCTAACATCTCAAGTC 27			
ORGANISM	Mus musculus			
MATERIALS	Mus musculus			
REFERENCE	1. (bases 1 to 49)			
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
FEATURES				
SOURCE				</td

Laboratory Mouse DNA Resource (<http://wwwjax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GIL473214 [gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells and selected for ampicillin resistance.

ORIGIN

	Query Match	Match Score	Length	DB	Best Local Similarity	Score	DB	Length
Qy	3 AGCTAACATCTCCAGTC	13.2	50	11	83.3%	64.0%	12.8	32
Db	30 AGCTCACAGCTCCAGTC	0	0	0	0	87.5%	1.1e+05	0

RESULT 10

	Query Match	Match Score	Length	DB	Best Local Similarity	Score	DB	Length
Qy	2 GAGTAAACATCTCCA	1.7	0	0	14%	0	0	0
Db	8 GAGCAAGCTCTCCA	23	0	0	0	0	0	0

ORIGIN

	Query Match	Match Score	Length	DB	Best Local Similarity	Score	DB	Length
Qy	2 GAGTAAACATCTCCA	1.7	0	0	14%	0	0	0
Db	8 GAGCAAGCTCTCCA	23	0	0	0	0	0	0

DEFINITION

clone UGCIM009107 R, genomic survey sequence.

ACCESSION

AZ357818.1 GI:10471518

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 41)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingay,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

FEATURES

Source
1. .41
/organism="Mus musculus"
/mol_type="Genomic DNA"
/strain="C57BL/6J"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/db_xref="taxon:10090"
/clone="UGCIM009107"
/sex="Male"

COMMENT

Insert Length: 10000 Std Error: 0.00
Place: 0099 row: 1 column: 07
Seq primer: CACAGAAAACAGCTATGACC
Class: plasmid ends
High Quality sequence stop: 41.
Location/Qualifiers

REFERENCE

1. .41

AUTHORS

/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/sex="Male"

TITLE

/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/sex="Male"

JOURNAL

/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/sex="Male"

COMMENT

/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labs."
/sex="Male"

FEATURES

Source
1. .32
/organism="Zea mays"
/mol_type="Genomic DNA"
/cultivar="mixed background W22/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="4021 - Rescuemu Grid V"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuemu is 4.9 kb, modified maize Mu transposon
Mu elements insert post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers

COMMENT

/lab_host="DH10B"
/clone_id="4021 - Rescuemu Grid V"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuemu is 4.9 kb, modified maize Mu transposon
Mu elements insert post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers

FEATURES

Source
1. .32
/organism="Zea mays"
/mol_type="Genomic DNA"
/cultivar="mixed background W22/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="4021 - Rescuemu Grid V"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuemu is 4.9 kb, modified maize Mu transposon
Mu elements insert post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically-competent E. coli XL1-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Score 12.8%; DB 11; Length 41;
Best Local Similarity 87.5%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGCTTACATCTCCA 16
Db 24 GGGCTTACATCTCCA 9

RESULT 11
LOCUS CC795628 c
DEFINITION SALK_087613.35.10.x Arabidopsis thaliana genomic clone SALK_087613.35.10.x, genomic survey sequence.

ACCESSION CC795628
VERSION OSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; spermatophyta; Magnoliophyta; eudicotyledons; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 28)
AUTHORS Alonso,J.M., Lefebvre,T.J., Barajas,P., Chen,H., Chauk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 453 4100 x1752
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES Source
1. Location/Qualifiers

2. /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecoType="Col-0"
/db_xref="Taxon:3702"
/clone="SALK_087613.35.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match Score 12.6%; DB 12; Length 28;
Best Local Similarity 78.9%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTTACATCTCCA 19
Db 21 GAATCTTACATCCAACT 3

RESULT 12

LOCUS AI194779/c

DEFINITION AI194779
FRUCTOSB-1,6-BISPHOSPHATASE ; mRNA sequence.

ACCESSION AI194779

VERSION AI194779.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

MAMMALIA

Eutheria

Buarchontoglires

Glires

Rodentia

Sciurognathi

Muroidea

Murinae

Mus

Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WASHU-HRM1 Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (<http://image.llnl.gov>) for further information.

MGI:970770

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.

Location/Qualifiers

1. 34

/organisms="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1886146"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone lib="Sugano mouse liver mRNA"

/note="Organ: Liver; Vector: PMB18S-FL3; Site:1: DraIII (CACTGTGTC); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGGCGCTTTTTTTTTTTTTT); double-stranded cDNA was

ligated to a DraIII adaptor (TGTRGGCTACTGG), digested and cloned into distinct DraIII sites of the PMB18S-FL3 vector (5' site CACGTGTC, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCCTGCCTAAAAGCTGCC and 3' end primer GACCTGAGCTGAGCACR."

ORIGIN

Query Match Score 12.4%; DB 1; Length 34;

Best Local Similarity 92.9%; Pred. No. 1.8e+05;

Matches 13; Conservative 0; Mismatches 1;

Indels 0; Gaps 0;

Db 29 AGCTAAGCTCTCA 16

Qy 3 AGCTAAGCTCTCA 16

Db 29 AGCTAAGCTCTCA 16

RESULT 13

CZ917814

LOCUS	C2917814	28 bp	DNA	linear	GSS 08-AUG-2005
DEFINITION	4021007812-2BL_y1 4021 - Rescuemu Grid V Zea mays genomic sequence.				
ACCESSION	C2917814				
VERSION	GI:71936909				
KEYWORDS					
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	Walbot, V.				
AUTHORS					
TITLE	Maize genomic sequences found using engineered Rescuemu transposon				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Walbot, V. Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu				
	Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.				
	Plate: 4021007 row: A column: 12				
FEATURES	Class: transposon-tagged				
source	Location/Qualifiers				
	1..28				
	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/cultivar="mixed background W23/A188/B73/K55"				
	/db_xref="taxon:5577"				
	/feature_type="leaf"				
	/dev_stage="adult"				
	/lab_host="DH10B"				
	/clone_lib="4021 - Rescuemu Grid V"				
	/note="Organ: leaf; Vector: Rescuemu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site: http://www.mutransposon.org/project/Rescuemu/ . Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
FEATURES	source				
source	Organism				
	Mus musculus				
	Mus musculus (house mouse)				
RESULT	14				
LOCUS	B2381186/c	35 bp	DNA	linear	GSS 26-NOV-2002
DEFINITION	Arabidopsis thaliana genomic clone SALK_116379.23-70.x, genomic survey sequence.				
ACCESSION	GI:25474462				
VERSION	GI:2381186.1				
KEYWORDS	GSS				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; roids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	Alonso, J.M., Leibig, T.J., Barajas, P., Chen, H., Cheuk, R., Kim, C.J., Kim, C.J., Parker, H., Prednis, L., Gadriab, C., Jeske, A., Karnes, M., Shinn, P., Zimmerman, J., and Ecker, J.R.				
AUTHORS	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome				
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu				
	This is single pass sequence recovered from the left border of TDNA.				
CLASS	TDNA tagged.				
	Location/Qualifiers				
	1..35				
	/organism="Arabidopsis thaliana"				
	/mol_type="genomic DNA"				
	/ecotype="Col-0"				
	/db_xref="SAXON_3702"				
	/clones="SALK_116379.23-70.x"				
	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://SIGnAL.salk.edu/tdna_protocols.html "				
FEATURES	source				
source	Organism				
	Mus musculus				
	Mus musculus (house mouse)				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 11; Length 35;				
	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
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	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	Best Local Similarity 82.4%; Pred. No. 2.3e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 GGAGCTAACATCCTCCA 17				
Db	17 GGTCGTAATAGCTCCAA 1				
ORIGIN					
	Query Match Score 12.2; DB 13; Length 28;				
	Best Local Similarity 82.4%; Pred. No. 2.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
RESULT	15				
LOCUS	A2989635	37 bp	DNA	linear	

Seq primer: CGTGTGAAACGAGGCCAGT

Class: Plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

1 .37

/organism="Mus musculus"

/mol type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0273K06"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dmases/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (91|473214|9b|AF129071.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Score 12 2; DB 11; Length 37;
 Best Local Similarity 82.4%; Pred. No 2.36+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCAAAGTC 20

Db 2 GCTAACATCTCCCGCC 18

Search completed: May 21, 2006, 23:02:41
 Job time : 2201 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:08:44 ; Search time 115.5 Seconds (without alignments)

324.002 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaggtaacatctccaaatgc 20

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0\$ Maximum Match 100\$ Listing First 45 summaries

Database : Issued_Patents_NA.*

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 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB. seq;*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB. seq;*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/65 COMB. seq;*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB. seq;*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB. seq;*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB. seq;*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB. seq;*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RN COMB. seq;*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	69.0	25	3 US-09-396-196G-88907	Sequence 88907, A
2	13.8	69.0	25	3 US-09-396-196G-88908	Sequence 88908, A
3	13.6	68.0	30	5 US-09-501-328-19	Sequence 19, App1
c 4	13.6	68.0	40	3 US-09-114-116-19	Sequence 19, App1
5	13.6	68.0	41	3 US-09-014-116-50	Sequence 50, App1
6	13.6	68.0	42	3 US-09-014-116-51	Sequence 51, App1
7	13.4	67.0	20	3 US-09-198-52A-110	Sequence 310, App1
c 8	13.4	67.0	25	3 US-09-396-196G-87226	Sequence 87226, A
9	13	65.0	25	3 US-09-396-196G-88906	Sequence 88906, A
c 10	12.8	64.0	24	3 US-10-002-074-76	Sequence 76, App1
c 11	12.8	64.0	24	3 US-10-002-074-77	Sequence 77, App1
c 12	12.8	64.0	29	3 US-09-214-218-13	Sequence 194, App1
c 13	12.8	64.0	47	3 US-09-422-078-1943	Sequence 4910, Ap
c 14	12.8	64.0	50	3 US-10-131-027-4910	Sequence 4910, Ap
c 15	12.8	64.0	50	5 US-10-131-031-4910	Sequence 4910, Ap
c 16	12.6	63.0	21	3 US-09-657-072-2547	Sequence 2547, Ap
c 17	12.6	63.0	25	3 US-09-396-196G-25961	Sequence 25961, A
c 18	12.6	63.0	25	3 US-09-396-196G-74047	Sequence 74047, A
c 19	12.6	63.0	26	3 US-09-014-116-18	Sequence 18, App1
c 20	12.6	63.0	30	4 US-10-206-06A-20	Sequence 20, App1
c 21	12.6	63.0	38	3 US-09-474-332B-1384	Sequence 1384, Ap
c 22	12.6	63.0	38	3 US-09-476-187-1383	Sequence 1383, Ap
c 23	12.6	63.0	39	2 US-08-537-002A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-396-196G-88907 ; Sequence 88907, Application US/09396196G
 ; Patent No. 6821724 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; ATTORNEY: David Mack
 ; ATTORNEY: David Lockhart
 ; ATTORNEY: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO: 88907
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 ; US-09-396-196G-88907

Query Match 69.0%; Score 13.8; Pred. No. 1.1e+03; DB 3; Length 25;
 Best Local Similarity 88.2%; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCTAACATCCAGTC 20
 Db 7 GCTAACATCCAGTC 23

RESULT 2

US-09-396-196G-88908 ; Sequence 88908, Application US/09396196G
 ; Patent No. 6821724 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; ATTORNEY: David Mack
 ; ATTORNEY: David Lockhart
 ; ATTORNEY: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 88908
 LENGTH: 25
 TYPE: DNA
 ORGANISM: *mus musculus*
 US-09-396-196G-88908

Query Match Score 68.0%; Best Local Similarity 80.0%; Pred. No. 1.5e+03; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
 Matches 16; Length 40;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 33 GGAGCTAACACTCCAGGCC 14

RESULT 5
 US-09-014-416-50
 Sequence 50, Application US/09014416
 Patent No. 6153421
 GENERAL INFORMATION:
 APPLICANT: Yanagi, Masayuki
 ATTORNEY: Bukh, Jens
 APPLICANT: Emerson, Susanne U.
 APPLICANT: Purcell, Robert H.
 TITLE OF INVENTION: CLONED GENOMES OF INFECTION HEPATITIS C VIRUSES AND FILE REFERENCE: 20264276
 CURRENT APPLICATION NUMBER: US/09/014,416
 EARLIER APPLICATION NUMBER: US 60/053,062
 EARLIER FILING DATE: 1998-01-27
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 50
 LENGTH: 41
 TYPE: DNA
 ORGANISM: Hepatitis C virus
 US-09-014-416-50

Query Match Score 68.0%; Best Local Similarity 80.0%; Pred. No. 1.5e+03; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
 Matches 16; Length 41;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 33 GGAGCTAACACTCCAGGCC 14

RESULT 6
 US-09-014-416-51
 Sequence 51, Application US/09014416
 Patent No. 6153421
 GENERAL INFORMATION:
 APPLICANT: Yanagi, Masayuki
 ATTORNEY: Bukh, Jens
 APPLICANT: Emerson, Susanne U.
 APPLICANT: Purcell, Robert H.
 TITLE OF INVENTION: CLONED GENOMES OF INFECTION HEPATITIS C VIRUSES AND FILE REFERENCE: 20264276
 CURRENT APPLICATION NUMBER: US/09/014,416
 EARLIER APPLICATION NUMBER: US 60/053,062
 EARLIER FILING DATE: 1998-01-27
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 51
 LENGTH: 42
 TYPE: DNA
 ORGANISM: Hepatitis C virus
 US-09-014-416-51

Query Match Score 68.0%; Best Local Similarity 80.0%; Pred. No. 1.5e+03; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
 Matches 16; Length 42;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 33 GGAGCTAACACTCCAGGCC 14

RESULT 7
US-09-198-452A-3110
 Sequence 3110; Application US/09198452A
 Patent No. 6559294
 GENERAL INFORMATION:
 APPLICANT: Griffais, R.
 TITLE OR INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
 FILE REFERENCE: 9710-003-999
 CURRENT FILING DATE: 1998-11-24
 SEQ ID NO 3110
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-3110

Query Match 67.0%; Score 13.4%; DB 3; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 GCTGACATCTCCAG 20

RESULT 8
US-09-396-196G-87226/C
 Sequence 87226; Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101_1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 87226
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-87226

Query Match 67.0%; Score 13.4%; DB 3; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 GAGCTAACATCTCCA 16
 22 GAGCTAAGCTCCA 8

RESULT 9
US-09-396-196G-88906
 Sequence 88906; Application US/09396196G
 Patent No. 6811724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101_1

CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 NUMBER OF SEQ ID NOS: 12786
 SEQ ID NO 88906
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-88906

Query Match 65.0%; Score 13.; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCTAACATCTCCA 16
 Db 13 GCTAACATCTCCA 25

RESULT 10
US-10-002-974-76/C
 Sequence 76; Application US/10002974
 Patent No. 6858391
 GENERAL INFORMATION:
 APPLICANT: Nunes, Gabriel
 APPLICANT: Inohara, Nachiro
 APPLICANT: Ogur, Yasunori
 APPLICANT: Cho, Judy
 APPLICANT: Nicolae, Dan L
 APPLICANT: Bonen, Denise
 TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
 FILE REFERENCE: UM-06646

CURRENT APPLICATION NUMBER: US/10/002, 974
 CURRENT FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 99
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 76

Query Match 64.0%; Score 12.8.; DB 3; Length 24;
 Best Local Similarity 87.5%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCA 17
 Db 16 GAGCTAACATCTGCCA 1

RESULT 11
US-10-002-974-77/C
 Sequence 77; Application US/10002974
 Patent No. 6858391
 GENERAL INFORMATION:
 APPLICANT: Nunes, Gabriel
 APPLICANT: Inohara, Nachiro
 APPLICANT: Ogur, Yasunori
 APPLICANT: Cho, Judy
 APPLICANT: Nicolae, Dan L
 APPLICANT: Bonen, Denise
 TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
 FILE REFERENCE: UM-06646

CURRENT APPLICATION NUMBER: US/10/002, 974
 CURRENT FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 99
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 77

Query Match 64.0%; Score 12.8.; DB 3; Length 24;
 Best Local Similarity 87.5%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCA 17
 Db 16 GAGCTAACATCTGCCA 1

ORGANISM: Homo sapiens
 US-10-002-974-77

Query Match Score 12.8; DB 3; Length 24;
 Best Local Similarity 87.5%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

Qy 2 GAGCTTACATCTCCAA 17
 Db 16 GAGCTTACATCTCCAA 1

RESULT 12
 US-09-214-718-13
 / Sequence 13, Application US/09214718
 / Patent No. 6756357
 / GENERAL INFORMATION:
 / APPLICANT: Laufer, Ralph
 / APPLICANT: Di Marco, Annalise
 / TITLE OF INVENTION: VARIANT OF HUMAN CILIARY NEUROTROPHIC FACTOR (HCNTF) WITH A RANGE OF ACTION DIFFERENT FROM THAT OF THE WILD-TYPE MOLECULE
 / TITLE OF INVENTION: THE WILD-TYPE MOLECULE
 / FILE REFERENCE: ITRO009P
 / CURRENT APPLICATION NUMBER: US/09/214,718
 / PRIOR APPLICATION NUMBER: PCT/IT97/00163
 / CURRENT FILING DATE: 1999-07-06
 / PRIOR FILING DATE: 1997-07-10
 / PRIOR APPLICATION NUMBER: RM96A000492
 / PRIOR FILING DATE: 1996-07-10
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 13
 / LENGTH: 29
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Primer
 US-09-214-718-13

Query Match Score 12.8; DB 3; Length 29;
 Best Local Similarity 87.5%; Pred. No. 3.6e+03;
 Matches 14; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

Qy 2 GAGCTTACATCTCCAA 17
 Db 13 GAGCTTACATCTCCAA 28

RESULT 13
 US-09-422-978-1943/C
 / Sequence 1943, Application US/09422978
 / Patent No. 6537751
 / GENERAL INFORMATION:
 / APPLICANT: Cohen, Daniel
 / APPLICANT: Blumanfield, Marla
 / APPLICANT: Chumakov, Ilya
 / TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 / FILE REFERENCE: GBNSFT-0205P1
 / CURRENT APPLICATION NUMBER: US/09/422,978
 / CURRENT FILING DATE: 1999-10-20
 / EARLIER APPLICATION NUMBER: US 09/298,850
 / EARLIER FILING DATE: 1999-04-21
 / EARLIER APPLICATION NUMBER: US 60/109,732
 / EARLIER FILING DATE: 1998-11-23
 / EARLIER APPLICATION NUMBER: US 60/082,614
 / EARLIER FILING DATE: 1998-04-21
 / NUMBER OF SEQ ID NOS: 11796
 / SEQ ID NO: 1943
 / LENGTH: 47
 / TYPE: DNA
 / ORGANISM: Homo Sapiens
 / FEATURE:
 / NAME/KEY: allele

RESULT 14
 US-10-131-827-4910/c
 / Sequence 4910, Application US/10131827
 / Patent No. 6905827
 / GENERAL INFORMATION:
 / APPLICANT: Wohlgemuth, Jay
 / APPLICANT: PTY, Kirk
 / APPLICANT: Woodward, Robert
 / APPLICANT: Ly, Ngoc
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 / CURRENT APPLICATION NUMBER: US/10/131,827
 / CURRENT FILING DATE: 2002-09-06
 / PRIOR APPLICATION NUMBER: US 10/006,290
 / PRIOR FILING DATE: 2001-10-22
 / PRIOR APPLICATION NUMBER: US 60/295,764
 / PRIOR FILING DATE: 2001-06-08
 / NUMBER OF SEQ ID NOS: 9090
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 4910
 / LENGTH: 50
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / OTHER INFORMATION: None
 US-10-131-827-4910

RESULT 15
 US-10-131-831-4910/c
 / Sequence 4910, Application US/10131831
 / Patent No. 7026121
 / GENERAL INFORMATION:
 / APPLICANT: Wohlgemuth, Jay
 / APPLICANT: PTY, Kirk
 / APPLICANT: Woodward, Robert
 / APPLICANT: Ly, Ngoc
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPLANT REJECTION
 / CURRENT APPLICATION NUMBER: US/06612000121
 / CURRENT FILING DATE: 2002-08-05
 / PRIOR APPLICATION NUMBER: US 10/131,831
 / PRIOR FILING DATE: 2001-10-22
 / PRIOR APPLICATION NUMBER: US 60/296,764
 / PRIOR FILING DATE: 2001-06-08
 / NUMBER OF SEQ ID NOS: 9190
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 4910
 / LENGTH: 50
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / OTHER INFORMATION: None
 US-10-131-831-4910

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Query Match 64.0%; Score 12.8; DB 5;
Best Local Similarity 87.5%; Pred. No. 3.9+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GAGCTAACATCTCAA 17
Db      32 GAGCTAACATCTCAA 17
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Search completed: May 21, 2006, 23:25:17
Job time : 116.5 SECs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:09:18 ; Search time: 654 Seconds
(without alignments)
375.769 Million cell updates/sec

Title: US-10-766-185-4
Perfect score: 20
Sequence: 1 ggaggtaacatctccaaatgc 20

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:
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 3: /EMC_Celerra_SIDS3/podata/2/pubpna/US09_PUBCOMB.seq*
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 7: /EMC_Celerra_SIDS3/podata/2/pubpna/US10_PUBCOMB.seq*
 8: /EMC_Celerra_SIDS3/podata/2/pubpna/US10C_PUBCOMB.seq*
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 12: /EMC_Celerra_SIDS3/podata/2/pubpna/US10H_PUBCOMB.seq*
 13: /EMC_Celerra_SIDS3/podata/2/pubpna/US11A_PUBCOMB.seq*
 14: /EMC_Celerra_SIDS3/podata/2/pubpna/US11C_PUBCOMB.seq*
 15: /EMC_Celerra_SIDS3/podata/2/pubpna/US11E_PUBCOMB.seq*
 16: /EMC_Celerra_SIDS3/podata/2/pubpna/US11D_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	20	100.0	20	8 US-10-766-185-4	Sequence 4, Appli
c 3	16	80.0	16	8 US-10-766-185-13	Sequence 13, Appli
c 4	15.8	79.0	25	8 US-10-719-936-576763	Sequence 576763,
c 5	15.8	79.0	25	9 US-10-719-900-163104	Sequence 163104,
c 6	15.4	77.0	25	9 US-10-719-900-213846	Sequence 213846,
c 7	15.4	77.0	25	11 US-10-932-182A-3140	Sequence 23140, A
c 8	15.2	76.0	25	11 US-10-932-182A-107428	Sequence 107428,
c 9	15.2	76.0	25	13 US-11-036-117-197855	Sequence 197855,
c 10	15.2	76.0	25	13 US-11-036-117-229502	Sequence 229502,
c 11	15.2	76.0	25	13 US-11-036-117-232030	Sequence 232030,
c 12	15.2	76.0	25	13 US-11-036-117-321919	Sequence 321919,
c 13	15.2	76.0	25	15 US-11-121-049-110453	Sequence 110453,
c 14	15	75.0	50	16 US-11-175-859-1271671	Sequence 56177,
c 15	14.8	74.0	19	14 US-11-083-784-429065	Sequence 429065,
c 16	14.8	74.0	19	14 US-11-083-784-1271642	Sequence 1271642,
c 17	14.8	74.0	19	15 US-11-101-244-429065	Sequence 429065,

ALIGNMENTS

RESULT 1	US-10-766-185-3/C	RESULT 2	US-10-766-185-4
/ Sequence 3, Application US/10766185	; Sequence 3, Application US/10766185	/ Sequence 4, Application US/10766185	; Sequence 4, Application US/10766185
; Publication No. US20040152655A1			
; GENERAL INFORMATION:	; GENERAL INFORMATION:	; GENERAL INFORMATION:	; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong	; APPLICANT: Ahn, Chang Ho	; APPLICANT: Lee, Young Bok	; APPLICANT: Lee, Young Bok
; INVENTION: Antisense Oligonucleotides that inhibit expression of HIV-1	; INVENTION: Antisense Oligonucleotides that inhibit expression of HIV-1	; INVENTION: Antisense Oligonucleotides that inhibit expression of HIV-1	; INVENTION: Antisense Oligonucleotides that inhibit expression of HIV-1
; PUBLISHER: REX 7034	; CURRENT APPLICATION NUMBER: US/10/766,185	; CURRENT APPLICATION NUMBER: US/10/766,185	; CURRENT APPLICATION NUMBER: US/10/766,185
; PUBLISHING DATE: 2004-01-28			
; NUMBER OF SEQ ID NOS: 130			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO: 3			
; LENGTH: 20	; LENGTH: 20	; LENGTH: 20	; LENGTH: 20
; TYPE: DNA	; TYPE: DNA	; TYPE: DNA	; TYPE: DNA
; ORGANISM: human	; ORGANISM: human	; ORGANISM: human	; ORGANISM: human

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; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-4

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGTAAACATCTCCAAAGTC 20
Db 1 GGAGTAAACATCTCCAAAGTC 20

RESULT 3
US-10-407-807-13
; Sequence 13. Application US/10407807
; Publication No. US2004096684A1
; GENERAL INFORMATION:
; APPLICANT: THRUR, CHARLOTTE ALBREK
; APPLICANT: HOG, ANJA MOLHART
; APPLICANT: KRISTJANSIN, PAUL E. G.
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION HIF-1ALPHA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 57390 (45120)
; CURRENT APPLICATION NUMBER: US/10/407,807
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/370,126
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn ver. 3.2
SEQ ID NO 13
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-407-807-13

Query Match 80.0%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GCTAACATCTCCAAAGTC 19
Db 1 GCTAACATCTCCAAAGTC 16

RESULT 4
US-10-719-956-576763/C
; Sequence 576763, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/422,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 6,9946
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
US-10-719-956-576763

Query Match 79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGCTAACATCTCCAAAGTC 20
Db 22 GAGGAACTTTCCAAAGTC 4

RESULT 5
US-10-719-900-163104/C
; Sequence 163104, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 163104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-163104

Query Match 79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAAGTC 19
Db 24 GAGGCAAACTTCGAACTCGAACT 6

RESULT 6
US-10-719-900-213846/C
; Sequence 213846, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 213846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-213846

Query Match 77.0%; Score 15.4; DB 9; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GCTAACATCTCCAAAGTC 20
Db 24 GCTAACATCTCCAAAGTC 8

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RESULT 7
US-10-932-182A-23140
Sequence 21140, Application US/10932182A
GENERAL INFORMATION:
SEQ ID NO: US20060046253A1
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISSA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932-182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 231140
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
US-10-932-182A-23140

Query Match 77.0%; Score 15.4%; DB 11; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCTAACATTCAGTCCAGTC 20
Db 5 GCTAAGATCTCCAGTC 21

RESULT 8
US-10-932-182A-107428
Sequence 107428, Application US/10932182A
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISSA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932-182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 107428
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
US-10-932-182A-107428

Query Match 76.0%; Score 15.2%; DB 11; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATTCAGTC 20
Db 5 GTGTGAAGATCAGTC 24

RESULT 9
US-10-036-317-197855/C
Sequence 197855, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Blume, John
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036-317
CURRENT FILING DATE: 2005-01-13
NUMBER OF SEQ ID NOS: 197023

Query Match 76.0%; Score 15.2%; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690-1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIORITY NUMBER: US 60/585,352
; PRIORITY FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 56177
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
; US-11-175-859-56177

RESULT 12
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654-1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIORITY NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 321919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-321919

Query Match 76.0%; Score 15.2; DB 13; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Query 1 GGAGCTAACATCTCCAAGTC 20
Db 21 GGAGATGACATGTCAGTC 2

RESULT 13
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3664-1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIORITY NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 110453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-110453

Query Match 76.0%; Score 15.2; DB 15; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Query 2 GAGCTAACATCTCCAAGT 19
Db 1 GAGCTAACATCTCCAAGT 18

RESULT 15
; Sequence 429065, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacor, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarine, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIORITY NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIORITY NUMBER: 60/502,050
; PRIORITY NUMBER: 60/426,137
; PRIORITY NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 429065
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-429065

Query Match 74.0%; Score 14.8; DB 14; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Query 2 GAGCTAACATCTCCAAGT 19
Db 1 GAGCTAACATCTCCAAGT 18

Search completed: May 21, 2006 22:32:00

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OM nucleic - nucleic search, using sw model.

Run on: May 21, 2006, 22:18:38 ; Search time 32.5 Seconds
(without alignments)

43.419 Million cell updates/sec

Title: US-10-766-185-4

Prefect score: 20

Sequence: 1 ggagtaaacatctccaaatgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Scanned: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 387544

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 10% Listing First 45 summaries.

Database : Published Applications_NA_New;*

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4: /EMC_Celerra_SIDS3/_prodatta/2/_pubpna/_US08_NEW_PUB.seq;*

5: /EMC_Celerra_SIDS3/_prodatta/2/_pubpna/_PCT_NEW_PUB.seq;*

6: /EMC_Celerra_SIDS3/_prodatta/2/_pubpna/_US10_NEW_PUB.seq;*

7: /EMC_Celerra_SIDS3/_prodatta/2/_pubpna/_US11_NEW_PUB.seq;*

8: /EMC_Celerra_SIDS3/_prodatta/2/_pubpna/_US60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	15.4	77.0	25	7 US-11-217-529-23140 Sequence 23140, A
2	15.2	76.0	25	7 US-11-217-529-23140 Sequence 107428, A
3	14	70.0	25	7 US-11-217-529-35122 Sequence 35122, A
4	13.8	69.0	25	7 US-11-217-529-70037 Sequence 70037, A
5	13.8	69.0	25	7 US-11-217-529-85327 Sequence 85327, A
6	13.6	68.0	25	7 US-11-217-529-46511 Sequence 46511, A
c	7	66.0	25	7 US-11-217-529-134913 Sequence 134913, A
c	8	12.8	64.0	25 US-11-217-529-8091 Sequence 8091, Ap
c	9	12.8	64.0	25 US-11-217-529-191839 Sequence 191839, Ap
c	10	12.8	64.0	50 6 US-11-217-529-2714 Sequence 2714, Ap
c	11	12.6	63.0	25 7 US-11-217-529-46527 Sequence 46527, A
c	12	12.6	63.0	25 7 US-11-217-529-84789 Sequence 84789, A
c	13	12.6	63.0	25 7 US-11-217-529-129113 Sequence 129113, A
c	14	12.6	63.0	25 7 US-11-217-529-141646 Sequence 141646, A
c	15	12.6	63.0	25 7 US-11-217-529-170895 Sequence 170895, A
c	16	12.6	63.0	27 US-09-156-097B-97 Sequence 97, App
c	17	12.6	63.0	30 1 US-09-156-097B-94 Sequence 94, App
c	18	12.4	62.0	25 7 US-11-217-529-978 Sequence 9788, Ap
c	19	12.4	62.0	25 7 US-11-217-529-23135 Sequence 23135, A
c	20	12.4	62.0	25 7 US-11-217-529-117896 Sequence 117896, A
c	21	12.4	62.0	34 6 US-10-946-650-26 Sequence 26, App
c	22	12.2	61.0	21 7 US-11-364-74-183 Sequence 183, App
c	23	12.2	61.0	25 7 US-11-217-529-9412 Sequence 9472, Ap
c	24	12.2	61.0	25 7 US-11-217-529-28702 Sequence 28702, A
c	25	12.2	61.0	25 7 US-11-217-529-33496 Sequence 33496, A

ALIGNMENTS

RESULT 1
US-11-217-529-23140

; Sequence 23140, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAMURA, YOSHIHARO

; APPLICANT: NAKAMURA, NORIHIRO

; APPLICANT: FUJIMURA, YUKIKO

; APPLICANT: ASHIKARI, TOMOKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11-217-529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197033

; SEQ ID NO: 23140

; LENGTH: 25

; TYPE: DNA

; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-23140

RESULT 2
US-11-217-529-107428

; Sequence 107428, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAMURA, YOSHIHARO

; APPLICANT: NAKAMURA, NORIHIRO

; APPLICANT: FUJIMURA, YUKIKO

; APPLICANT: ASHIKARI, TOMOKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217-529

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// CURRENT FILING DATE: 2005-09-02
// PRIOR APPLICATION NUMBER: US 10/932,182
// PRIORITY FILING DATE: 2004-09-02
// NUMBER OF SEQ ID NOS: 197023
// SEQ ID NO: 107428
// TYPE: DNA
// ORGANISM: Saccharomyces pastorianus
// US-11-217-529-107428

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 7; 7;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCCAACTC 20
Db 5 GGTGCTAAGATCACCAAGTC 24

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RESULT 5
US-11-217-529-85327
Sequence 85327, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
FILE REFERENCE: S-38-285
SEQUENCE 35122, Application US/11217529
PUBLICATION NO. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
FILE REFERENCE: S-38-285
APPLICANT: NAKAMURA, NORIHIRO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35122
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
// US-11-217-529-35122

Query Match 70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 32; 7;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 AACATCTCCAACTC 20
Db 4 AACATCTCCAACTC 17

RESULT 6
US-11-217-529-46511
Sequence 46511, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
FILE REFERENCE: S-38-285
SEQUENCE 35122, Application US/11217529
PUBLICATION NO. US20060099612A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA, NORIHIRO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 46511
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
// US-11-217-529-46511

RESULT 4
US-11-217-529-70037
Sequence 70037, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 46511
LENGTH: 25
TYPE: DNA
ORGANISM: *Saccharomyces pastorianus*
// US-11-217-529-46511

Query Match 68.0%; Score 13.6; DB 7; Length 25;
 Best Local Similarity 80.0%; Pred. No. 51;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCAAAGTC 20
 Db 1 GGAACTAACGCTGCAAGGC 20

RESULT 7
 US-11-217-529-134913/c
 Sequence 134913, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 / APPLICANT: SUNTORY LIMITED
 / APPLICANT: NAKAO, YOSHIIRO
 / APPLICANT: NAKAMURA, NORIHISA
 / APPLICANT: KODAMA, YUKIKO
 / APPLICANT: FUJIMURA, TOMOKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / APPLICANT: NAKAMURA, NORIHISA
 / APPLICANT: KODAMA, YUKIKO
 / APPLICANT: FUJIMURA, TOMOKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 / FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 PRIORITY APPLICATION NUMBER: US/04-09-02
 CURRENT FILING DATE: 2005-09-02
 PRIORITY APPLICATION NUMBER: US 10/932,182
 PRIORITY FILING DATE: 2004-09-02
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 134913
 LENGTH: 25
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-134913

Query Match 66.0%; Score 13.2; DB 7; Length 25;
 Best Local Similarity 83.3%; Pred. No. 82;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGCTCATACATGCCAAAGT 19
 Db 23 GAGAAACATGCCAAAGT 6

RESULT 8
 US-11-217-529-8091/c
 Sequence 8091, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 / APPLICANT: SUNTORY LIMITED
 / APPLICANT: NAKAO, YOSHIIRO
 / APPLICANT: NAKAO, YOSHIIRO
 / APPLICANT: FUJIMURA, TOMOKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 / FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY APPLICATION NUMBER: US 10/932,182
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 8091
 LENGTH: 25
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-8091

Query Match 64.0%; Score 12.8; DB 7; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCTAACATCTCCAAG 18
 Db 19 AGCTAACATCTCCAAG 4

RESULT 9
 US-11-217-529-191839/c
 Sequence 191839, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 / APPLICANT: SUNTORY LIMITED
 / APPLICANT: NAKAO, YOSHIIRO
 / APPLICANT: NAKAMURA, NORIHISA
 / APPLICANT: KODAMA, YUKIKO
 / APPLICANT: FUJIMURA, TOMOKO
 / APPLICANT: ASHIKARI, TOSHIHIKO
 / TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 / FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY APPLICATION NUMBER: US 10/932,182
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 191839
 LENGTH: 25
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-191839

Query Match 64.0%; Score 12.8; DB 7; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCTAACATCTCCAAG 18
 Db 21 AGCTAACAGCTACAAG 6

RESULT 10
 US-10-511-937-2714/c
 Sequence 2714, Application US/10511937
 Publication No. US20060088886A1
 GENERAL INFORMATION:
 / APPLICANT: EXPRESSION DIAGNOSTICS, INC.
 / APPLICANT: Wohlgemuth, Jay
 / APPLICANT: FRY, Kirk
 / APPLICANT: Woodward, Robert
 / APPLICANT: LY, Ngoc
 / APPLICANT: Prentice, James
 / APPLICANT: Morris, MacDonald
 / APPLICANT: Rosenberg, Steven
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSTICING
 / FILE REFERENCE: 506612000104
 CURRENT APPLICATION NUMBER: US/10/511,937
 CURRENT FILING DATE: 2004-10-19
 PRIORITY APPLICATION NUMBER: PCT/US2003/012346
 PRIORITY FILING DATE: 2003-04-24
 PRIORITY APPLICATION NUMBER: US 10/131,831
 PRIORITY FILING DATE: 2002-04-24
 PRIORITY APPLICATION NUMBER: US 10/325,899
 PRIORITY FILING DATE: 2002-12-20
 NUMBER OF SEQ ID NOS: 3117
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2714
 LENGTH: 50
 TYPE: DNA
 ORGANISM: *Homo sapiens*
 US-10-511-937-2714

Query Match 64.0%; Score 12.8; DB 6; Length 50;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GAGCTAACATCTCCAA 17
 Db 32 GAGCTAACATCTCCAA 17

RESULT 11
 US-11-217-529-46927
 ; Sequence 46927, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; PFILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 46927
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-46927

Query Match 63.0%; Score 12.6%; DB 7; Length 25;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAACT 19
 Db 2 GAGCTAACATCTCCAACT 20

RESULT 12
 US-11-217-529-84789
 ; Sequence 84789, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIWA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; PFILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 84789
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-84789

Query Match 63.0%; Score 12.6%; DB 7; Length 25;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAACT 19
 Db 5 GGATCTAACCTCACAACT 23

RESULT 13
 US-11-217-529-129113/C
 ; Sequence 129113, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIWA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; PFILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 129113
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-129113

Query Match 63.0%; Score 12.6%; DB 7; Length 25;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAACT 20
 Db 19 GAGCTAACATCTCCAACT 20

RESULT 14
 US-11-217-529-141646/C
 ; Sequence 141646, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIWA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; PFILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIORITY APPLICATION NUMBER: US 10/932,182
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 141646
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-141646

Query Match 63.0%; Score 12.6%; DB 7; Length 25;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAACT 20
 Db 23 GAGCTAACATCTCCAACT 23

RESULT 15
 US-11-217-529-170895/C
 ; Sequence 170895, Application US/11217529

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; NAKAO, YOSHIHARO
; NAKAMURA, NORIHISA
; KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 6-36-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 170895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*
us-11-217-529-170895

Query Match 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qry 2 GAGCTAACATCTCCAGTC 20
Db 21 GAGCTAACATCTCCAGTC 3

Search completed: May 21, 2006, 22:34:13
Job time : 33.5 secs

Run on:	May 21, 2006, 21:09:23 ; Search time 13:11 Seconds (without alignments) 960.893 Million cell updates/sec
Title:	US-10-766-185-4
Perfect score :	20
Sequence:	1 ggacgttaacatctccaaatgc 20
Scoring table:	IDENTITY_NUC
Gapcost:	10.0 , Gapext 1.0
Searched:	6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters:	12732272
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0% Maximum Match 100%
	Listing First 45 summaries
Database :	GenEmbl: 1: gb_env: 2: gb_pat: 3: gb_ph: 4: gb_pr: 5: gb_pr: 6: gb_pr: 7: gb_sub: 8: gb_sv: 9: gb_fn: 10: gb_v1: 11: gb_ov: 12: gb_ntg: 13: gb_in: 14: gb_cm: 15: gb_da: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
	GenEmbl: 1: gb_env: 2: gb_pat: 3: gb_ph: 4: gb_pr: 5: gb_pr: 6: gb_pr: 7: gb_sub: 8: gb_sv: 9: gb_fn: 10: gb_v1: 11: gb_ov: 12: gb_ntg: 13: gb_in: 14: gb_cm: 15: gb_da: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
	RESULTS
	BD187062
	LOCUS
	DEFINITION
	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.
	BD187062.1
	GI:31879262
	WO 02039104-A/22.
	KEYWORDS
	Synthetic construct
	ORGANISM
	synthetic construct
	other sequences; artificial sequences.
	REFERENCE
	AUTHORS
	Hiraoka, M., Kondo, S. and Harada, H.
	TITLE
	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it
	PATENT
	WO 02039104-A 22 12-DEC-2002;
	JOURNAL
	POLA CHEMICAL INDUSTRIES INC., MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA
	COMMENT
	OS Artificial sequence
	PN WO 02039104-A/22
	PD 12-DEC-2002
	PP 04-JUN-2002 WO 2002JB005482
	PR 05-JUN-2001 JP 01P 169949 PI
	MASAHIRO HIRAOKA, SHINAE KONDO, HIROSHI HARADA
	PC C12N15/09, C1Q1/68, C07K14/47, C07K19/00
	CC Description of Artificial Sequence: synthetic DNA PH Key
	FT Location/Qualifiers
	1. 49 source
	FT /organism='Artificial Sequence'.
	FT Location/Qualifiers
	1. .49
	/organism='Synthetic construct'
	/mol_type='Genomic DNA'
	/db_xref='taxon:32630'
	ORIGIN
	Query Match 100.0%; Score 20; DB 2; Length 49;
	Best Local Similarity 100.0%; Pred. No. 17;
	Matches 20; Conservative 0; Mismatches 0; Gaps 0;
	Indels 0;
	Y 1 GGAGCTAACATCTCCAAGTC 20

Db	26	GGAGCTAACATCTCCAGTC	45		PC	C12N15/09,C12Q1/68,C07K14/47,C07K19/00		
					CC	Description of Artificial Sequence: synthetic DNA	FH	Key
RESULT 2					FT	Source	1..57	
BD187041/c					FT	Location/Qualifiers		
LOCUS			54 bp	DNA	FT			
DEFINITION			linear	PAT 17-JUN-2003				
Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.								
ACCESSION	BD187041							
VERSION	1	GI:	31879241					
KEYWORDS	WO 02099104-A/1.							
SOURCE								
ORGANISM								
Synthetic construct								
Other sequences; artificial sequences.								
RBRFERENCE								
AUTHORS	Hiraoka, M., Kondo, S. and Harada, H.							
TITLE	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it							
JOURNAL	Patent: WO 02099104-A 1 12-DEC-2002;							
	POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAKA, SHINAE KONDO, HIROSHI HARADA							
COMMENT								
	OS Artificial Sequence							
	PN WO 02099104-A/1							
	PP 12-DEC-2002							
	PR 04-JUN-2002 WO 2002JP005482							
	PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI							
	PC MASAHIRO HIRAKA, SHINAE KONDO, HIROSHI HARADA							
	PC C12N15/09,C12Q1/68,C07K14/47,C07K19/00							
	CC Description of Artificial Sequence: synthetic DNA							
	Key Location/Qualifiers							
	FT source 1..54							
	FT /organism=,Artificial Sequence.							
	FEATURES source 1..54							
	/organism="synthetic construct"							
	/mol_type="genomic DNA"							
	/db_xref="taxon:32630"							
ORIGIN								
	Query Match 100.0%		Score 20;	DB 2;	Length 54;			
	Best Local Similarity 100.0%		Pred. No. 17;					
	Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1	GGAGCTAACATCTCCAGTC	20					
Db	23	GGAGCTAACATCTCCAGTC	4					
RESULT 3								
BD187061/c		BD187061						
LOCUS			57 bp	DNA				
DEFINITION			linear	PAT 17-JUN-2003				
Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.								
ACCESSION	BD187061							
VERSION	1	GI:	31879261					
KEYWORDS	WO 02099104-A/21.							
SOURCE								
ORGANISM								
Synthetic construct								
Other sequences; artificial sequences.								
RBRFERENCE								
AUTHORS	Hiraoka, M., Kondo, S. and Harada, H.							
TITLE	Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it							
JOURNAL	Patent: WO 02099104-A 21 12-DEC-2002;							
	POLA CHEMICAL INDUSTRIES INC, MASAHIRO HIRAKA, SHINAE KONDO, HIROSHI HARADA							
COMMENT								
	OS Artificial Sequence							
	PN WO 02099104-A/21							
	PP 12-DEC-2002							
	PR 04-JUN-2002 WO 2002JP005482							
	PR 05-JUN-2001 JP 01P 169948, 05-JUN-2001 JP 01P 169949 PI							
	PC MASAHIRO HIRAKA, SHINAE KONDO, HIROSHI HARADA							
	CC Description of Artificial Sequence: synthetic DNA							
	FH Key Location/Qualifiers							
	FT source 1..58							
	FT /organism=,Artificial Sequence.							
	FEATURES source 1..58							
	/organism="synthetic construct"							
	/mol_type="genomic DNA"							
	/db_xref="taxon:32630"							
ORIGIN								
	Query Match 100.0%		Score 20;	DB 2;	Length 58;			
	Best Local Similarity 100.0%		Pred. No. 17;					
	Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1	GGAGCTAACATCTCCAGTC	20					
Db	23	GGAGCTAACATCTCCAGTC	4					
RESULT 5								
BD187066								
LOCUS			58 bp	DNA				
DEFINITION			linear	PAT 17-JUN-2003				
Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.								
ACCESSION	BD187066							
VERSION	1	GI:	31879266					

KEYWORDS WO 02099104-A/26.

SOURCE Synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 58)

AUTHORS Hiroka,M., Kondo,S. and Harada,H.

TITLE Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it

JOURNAL Patent. WO 02099104-A 26 12-DEC-2002;

COMMENT POLA CHEMICAL INDUSTRIES INC.,MASAHIRO HIRAKA,SHINAE KONDO, HIROSHI HARADA

OS Artificial Sequence

PN WO 02099104-A/26

PD 12-DEC-2002

PF 04-JUN-2002 WO 2002JP005492

PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI

MASAHIRO HIRAKA,SHINAE KONDO,HIROSHI HARADA

FC C12N15/09,C12Q1/68,C07K14/47,C07K19/00

CC Description of Artificial Sequence: synthetic DNA FH Key

Location/Qualifiers

FT source 1..58 /organism='Artificial Sequence'.

FEATURES

Source

1..58 /organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Qy Query Match 100.0%; Score 20; DB 2; Length 58;

Db Best Local Similarity 100.0%; Pred. No. 17; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

CQ536778/C BD187057/c

LOCUS CQ536778 60 bp DNA

DEFINITION Sequence 6413 from Patent WO0210449.

ACCESSION CQ536778

VERSION CQ536778.1 GI:41503042

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.

AUTHORS Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome

TITLE Patent: WO 0210449-A 6413 07-FEB-2002;

JOURNAL Compugen Inc. (US)

FEATURES

Source

1..60 /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Qy Query Match 100.0%; Score 20; DB 2; Length 60;

Db Best Local Similarity 100.0%; Pred. No. 17; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

CQ536778/C BD187065/c

LOCUS CQ536778 60 bp DNA

DEFINITION Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.

ACCESSION BD187065

VERSION BD187065.1 GI:31179265

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 66)

AUTHORS Hiroka,M., Kondo,S. and Harada,H.

TITLE Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it

JOURNAL Patent: WO 02099104-A 25 12-DEC-2002;

COMMENT POLA CHEMICAL INDUSTRIES INC.,MASAHIRO HIRAKA,SHINAE KONDO, HIROSHI HARADA

OS Artificial Sequence

PN WO 02099104-A/25

PD 12-DEC-2002

PF 04-JUN-2002 WO 2002JP005482

PR 05-JUN-2001 JP 01P 169948,05-JUN-2001 JP 01P 169949 PI

MASAHIRO HIRAKA,SHINAE KONDO,HIROSHI HARADA

FC C12N15/09,C12Q1/68,C07K14/47,C07K19/00

CC Description of Artificial Sequence: synthetic DNA FH Key

Location/Qualifiers

FT source 1..66 /organism='Artificial Sequence'.

RESULT 7

FEATURES	source	Location/Qualifiers
		1..66 /organism="synthetic construct" /mol type="genomic DNA" /db_xref="taxon:32630"
ORIGIN		
Query Match		Score 20; DB 2; Length 66;
Best Local Similarity		100.0%; Pred. No. 18;
Matches 20;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	GGAGCTAACATCTCCAACTC 20
Db	28	GGAGCTAACATCTCCAACTC 9
RESULT 9		
BD187042/c		168 bp DNA linear PAT 17-JUN-2003
DEFINITION		Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it.
ACCESSION	BD187042	
VERSION	BD187042.1	GT;31879242
KEYWORDS	WO 02099104-A1/2.	
SOURCE		Synthetic construct
ORGANISM		Synthetic construct
		Other sequences; artificial sequences.
REFERENCE		1 (bases 1 to 168)
AUTHORS	Hirakawa,M., Kondo,S., and Harada,H.	
TITLE		Polypeptide causing protein unstable in cell under aerobic condition and DNA encoding it
JOURNAL		Patent: WO 02099104-A 2 1-DEC-2002; POLA CHEMICAL INDUSTRIES INC. MASAHIRO HIRAKAWA, SHINAE KONDO, HIROSHI HARADA
COMMENT		OS Artificial Sequence
PN	WO 02099104-A/2	
PD	12-DEC-2002	
PF	04-DEC-2002	WO 2002JP005482
PR	05-JUN-2001	JP 01P 163948, 05-JUN-2001 JP 01P
PC	C12N15/09, C12Q1/68	C07K14/47, C07K19/00
CC	Description of Artificial sequence: synthetic DNA FH	Key
		Location/Qualifiers
FT	source 1..168	/organism='Artificial Sequence'.
		Location/Qualifiers
FEATURES	source	1..168 /organism="synthetic construct" /mol type="genomic DNA" /db_xref="taxon:32630"
ORIGIN		
Query Match		Score 20; DB 2; Length 168;
Best Local Similarity		100.0%; Pred. No. 21;
Matches 20;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	GGAGCTAACATCTCCAACTC 20
Db	50	GGAGCTAACATCTCCAACTC 31
RESULT 10		
AY8428956/c		716 bp DNA linear MAM 20-JUN-2005
DEFINITION		Phoca hispida hypoxia-inducible factor 1alpha gene, exons 11..12 and partial cds.
ACCESSION		
VERSION		
KEYWORDS		
SEGMENT	6 of 7	
SOURCE	Phoca hispida (ringed seal)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Laurasiatheria; Carnivora; Pinnipedia; Phocidae; Phoca.		
REFERENCE	1 (bases 1 to 716)	
AUTHORS	Johnson,P., Elsner,R. and Zenteno-Savín,T.	
TITLE	Hypoxia-inducible Factor 1 in ringed seal (Phoca hispida) tissues	
JOURNAL	Free Radic. Res. 38 (8), 847-854 (2004)	
PUBMED	15493458	
REFERENCE	2 (bases 1 to 716)	
AUTHORS	Johnson,P., Elsner,R. and Zenteno-Savín,T.	
TITLE	Hypoxia-inducible factor 1 proteomics and diving adaptations in ringed seal	
JOURNAL	Free Radic. Biol. Med. 39 (2), 205-212 (2005)	
PUBMED	15564512	
REFERENCE	3 (bases 1 to 716)	
AUTHORS	Johnson,P., Elsner,R. and Zenteno-Savín,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-DEC-2004) Biomedical Sciences, Ohio University, Irvine Hall, Athens, OH 45701, USA	
FEATURES	source	
		1. .716 /organism="Phoca hispida"
		/mol type="genomic DNA"
		/db_xref="taxon:9118"
	mRNA	join(<87..209,341..>716)
	CDS	/product="hypoxia-inducible factor 1alpha"
		Join(<87..209,341..>716)
		/codon_start=1
		/product="hypoxia-inducible factor 1alpha"
		/protein_id=AAX4806.1"
		/db_xref="GI:61615856"
		/translation:"PNSPSBYCPDSDMMNEPKLFAEDTEAKNPESTQDTDLDLEMPLAPIPMDDDFQLRFDQLSPLESSSTSPPQASAKSPYSPDTGSRASPNAGKGVIETGD"
	exon	87..209
	exon	/number=1..1
		341..>716
		/number=12
	ORIGIN	
		Query Match 100.0%; Score 20; DB 14; Length 716;
		Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indexes 0; Gaps 0;
	Qy	1 GGAGCTAACATCTCCAACTC 20
	Db	372 GGAGCTAACATCTCCAACTC 353
RESULT 11		
HSHIF1A10/c		996 bp DNA linear PRI 26-OCT-1998
LOCUS		Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene, exons 11 and 12.
DEFINITION		
ORGANISM		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
KEYWORDS		1 (bases 1 to 996)
SOURCE		Iyer,N.V., Leung,S.W. and Semenza,G.L.
ORGANISM		The human hypoxia-inducible factor 1alpha gene: HIF1A structure and evolution
JOURNAL		Genomics 52 (2), 159-165 (1998)
PUBMED	9782081	
REFERENCE	2 (bases 1 to 996)	
AUTHORS	Iyer,N.V., Leung,S.W. and Semenza,G.L.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-FEB-1998) Departments of Pediatrics and Medicine,	

Db	1631 GGAGCTAACATCTCCAAAGTC 1612	FEATURES	Ribopharma AG (DE), Location/Qualifiers
RESULT 14		Source	1..2481
AX451938/C	AX451938 2481 bp DNA linear PAT 03-JUL-2002	ORGANISM	/organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
LOCUS	Sequence 3 from Patent WO0212326.	KEYWORDS	Query Match 100.0%; Score 20; DB 2; Length 2481;
DEFINITION		Match	Best Local Similarity 100.0%; Pred. No. 37;
ACCESSION		Matches	0; Mismatches 0; Indels 0; Gaps 0;
VERSION	AX451938.1 GI:21698761	Qy	1 GGAGCTAACATCTCCAAAGTC 20
SOURCE	Homo sapiens (human)	Db	1691 GGAGCTAACATCTCCAAAGTC 1672
ORGANISM	Homo sapiens	Search completed: May 21, 2006, 22:18:16	
	Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini; Hominidae; Homo.	Job time :	1333 secs
REFERENCE	1. Poellinger, L., Pereira, T., and Ruas, J.		
AUTHORS	Mechanism of conditional regulation of the hypoxia-inducible		
TITLE	factor-1 by the von Hippel-Lindau tumor suppressor protein		
JOURNAL	Patent: WO 0212326-A 3 14-FEB-2002;		
FEATURES	Angiotogenetics Sweden AB (SE)		
SOURCE			
1..2481			
/organism="Homo sapiens"			
/mol type="unassigned DNA"			
/db_xref="taxon:9606"			
CDS			
1..2481			
/note="unnamed protein product"			
/codon_start=1			
/protein_id="CAD37798.1"			
/db_xref="GI:21698762"			
/translation="MEGAGANDKKKISSERKEKSRSRKESEVFYLALHQVPLRHNVSFHLDKASYMRLLTSLYRLRKLLDAGLDIEDMKKAQNCFTYKALDFVMVLTDDGDMIVYSDNNVNKYMGTQFTHPCDHEBMRMLTHRLVYKGKESNTQTSPLAKMKTLSGRMTNISAKTVHLCTGHINVQDGCKKPMTCLVJCEPPLAKPSNTEIPLDKTFSLURSHLDKMFYKCDRIRTELMYBELLGRSITYEYHALDSDLKTKTHDMFVKGQVTGOTVMSLDRMKMKTQLPTKVESEDSSLDKLKKIVCVNYVSVGLIHDILPSLQQTCTVGLKPVBSLDRMKMKTQLPTKVESEDSSLDKLKKBDALTLAPAGDTISSLQFGNSNDTETDQQLBEEVPLNDVWLPSPNKLQLQINLAMSPPEAETPKPLRSADPALSNEVAKLLENPELSEFTMPQLQDOPSPSPSGSTROSSPPEENSPSEYCFYDSDMNEFEXKLEVECLAEADDTEAKNPSTODDIDLEMAYIPMDDFQLRFQDQSPLESSASPPASASPOSTVTFQQTQIQSPSTANATTATTDELKTVTDKDRMEDIKLJIASPSTHILKETTSATATSPTDOSRSPTRACKGVBEQTEKSHPPSPNVLSVALSORRTTYPPEELNPKLALQNKRMKMEHDSLFOQAVGIGTLLQQPDHAAHTSLSWRVYKGCKSSBQNEMBQKTLIIPSDLACRLQSMDSGLPOLTSDCEVNAPIQGSRNLIQGEERJRALDQVN"			
ORIGIN			
RESULT 15			
AX481424/C	AX481424 2481 bp DNA linear PAT 16-AUG-2002	FEATURES	Query Match 100.0%; Score 20; DB 2; Length 2481;
LOCUS	Sequence 38 from Patent WO02055693.	Match	Best Local Similarity 100.0%; Pred. No. 37;
DEFINITION		Matches	0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	AX481424	Qy	1 GGAGCTAACATCTCCAAAGTC 20
VERSION	AX481424.1 GI:22316338	Db	1691 GGAGCTAACATCTCCAAAGTC 1672
SOURCE	Homo sapiens (human)	Search completed: May 21, 2006, 22:18:16	
ORGANISM	Homo sapiens	Job time :	1333 secs
	Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini; Hominidae; Homo.		
REFERENCE	Kreutzer, R., Limmer, S., Rost, S., and Hadwiger, P.		
AUTHORS	Method for inhibiting the expression of a target gene		
TITLE	Patent: WO 02055693-A 38 18-JUL-2002;		
JOURNAL			

ALIGNMENTS

RESULT 1
ADQ88723/c

ADD088723;
21-OCT-2004 (first entry)
Human hypoxia inducible factor-1 gene fragment seqid 2.
RX-0047, RK-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
cancer; infection; inflammation; tumour formation; 86.
ADD088723;

ered. No. is the number of results predicted by chance to have a score greater than or equal to the observed one.

result	No.	Score	Query	Match	Length	DB	ID	Description
c	1	20	100.0	20	13	ADQ88723		Adq88723 Human hyp
c	2	20	100.0	20	13	ADQ88724		Adq88724 Human HIF
c	3	20	100.0	49	8	AB276611		Ab276611 Human HIF
c	4	20	100.0	54	8	AB271164		Ab271164 Hypoxia-1
c	5	20	100.0	57	8	AB276610		Ab276610 Human HIF
c	6	20	100.0	58	8	AB276615		Ab276615 Human HIF
c	7	20	100.0	58	8	AB276607		Ab276607 Human HIF
c	8	20	100.0	60	6	ABN31665		Abn31665 Human spl
c	9	20	100.0	60	8	AB271180		Ab271180 Human HIF
c	10	20	100.0	66	8	AB276614		Ab276614 Human HIF
c	11	20	100.0	168	8	AB271165		Ab271165 Human HIF
c	12	20	100.0	1335	4	AAP85323		Aap85323 Nucleotid
c	13	20	100.0	1354	14	AEC31706		Aec31706 Anoxia Co
c	14	20	100.0	2481	6	ABV78154		Abv78154 Human HIF
c	15	20	100.0	2481	6	AB235730		Ab235730 Human HIF
c	16	20	100.0	2481	6	ABK11552		Abk11552 Human CDN
c	17	20	100.0	2481	6	ABX09973		Abx09973 Human HIF
c	18	20	100.0	2481	6	ABL91695		Abl91695 Human HIF

Homo sapiens
US2004152655-A1.

PD	05-AUG-2004.
XX	
PP	28-JAN-2004; 2004US-00766185.
XX	
PR	31-JAN-2003; 2003US-0444367P.
XX	
PA	(YOUN/)
PA	YOON H.
PA	(MAOL/)
PA	MAO L.
PA	(LEEV/)
PA	LEE Y B.
PA	(AHNC/)
PA	AHN C.
PA	(JIAN/)
XX	JIANG X.
PI	Yoon H., Mao L., Lee YB., Ahn C., Jiang X;
XX	
WPI;	2004-561492/54.
XX	
PT	New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
PT	nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
PT	useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
PT	several cancer cells.
XX	
PS	Example 4: SEQ ID NO 3; 35pp; English.
XX	
XX	The invention describes a compound RX-0047 or RX-0149 targeted to a

nucleic acid molecule encoding human hypoxia inducible factor (HIF-1), where the oligonucleotide compound inhibits the expression of human HIF-1. Also described are: a method of inhibiting the expression of HIF-1 in human cells or tissues; and a method of inducing cytotoxicity in a cancer cell. Specifically claimed are RX-0047 and RX-0149 compounds having a fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5', attagccaccgttccaa 3', and SEQ ID NO. 4, 5', ggagctaacatccaaagt 3', respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The antisense compounds are also useful for preventing or delaying infection, inflammation, or tumour formation. This sequence represents a site on the HIF-1 to which antisense oligonucleotides can be targeted in order to control HIF-1 gene expression.

Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match Score 20 / DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCAAAGTC 20
Db 20 GGAGCTAACATCCAAAGTC 1

RESULT 3
ABZ76611 standard; DNA; 49 BP.

Qy ID ABZ76611
Db ID ABZ76611
XX AC ABZ76611;
XX DT 30-APR-2003 (first entry)
XX XX Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.
DB XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; Stabilisation; cytotoxic;
XX KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
XX KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
NLS; ODD; PCR Primer; 88.
XX OS Homo sapiens.
XX PN WO200299104-A1.
XX PR 05-JUN-2001; 2001JP-0016948.
XX PR 05-JUN-2001; 2001JP-0016949.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-0016948.
XX PA (POKK) POLA CHEM IND INC.
PA (HIRAKO /) HIRAKO M.
PA (KONDOKO /) KONDOKO S.
XX PI Hirakao M, Kondoh S, Harada H;
XX DR WPI; 2003-148670/14.
XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic PT conditions to proteins within the cell, useful for treatment of cancer PT and improvement of microbial fermentation.
XX Example: Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMALPYIMDDPQL see ABP57669) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cyostatic activity, and can be used for the

CC aatggagccaccgttccaa 3', and SEQ ID NO. 4, 5' ggagctaacatccaaagt 3', CC respectively). The compounds are useful for inhibiting the expression of HIF-1 and inducing the cytotoxicity in several cancer cells. The CC antisense compounds are also useful for preventing or delaying infection, CC inflammation, or tumour formation. This sequence represents a human HIF-1 CC antisense oligonucleotide.

XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match Score 20 / DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1 GGAGCTAACATCTCCAAAGTC 20

RESULT 3
ABZ76611 standard; DNA; 49 BP.

Qy ID ABZ76611
Db ID ABZ76611
XX AC ABZ76611;
XX DT 30-APR-2003 (first entry)
XX XX Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:24.
DB XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; Stabilisation; cytotoxic;
XX KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
XX KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
NLS; ODD; PCR Primer; 88.
XX OS Homo sapiens.
XX PN WO200299104-A1.
XX PR 05-JUN-2001; 2001JP-0016948.
XX PR 05-JUN-2001; 2001JP-0016949.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-0016948.
XX PA (POKK) POLA CHEM IND INC.
PA (HIRAKO /) HIRAKO M.
PA (KONDOKO /) KONDOKO S.
XX PI Hirakao M, Kondoh S, Harada H;
XX DR WPI; 2003-148670/14.
XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic PT conditions to proteins within the cell, useful for treatment of cancer PT and improvement of microbial fermentation.
XX Example: Page 24; 144pp; Japanese.

CC The present invention describes DNA encoding a hypoxia-inducible factor 1 CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMALPYIMDDPQL CC see ABP57669) (1), or encoding a fusion protein containing at least 16 CC residues of (1), a nuclear localisation signal (NLS), and another CC protein, and imparting relative stability under specific conditions of CC oxygen concentration within the cell. Also described: (1) vectors CC containing the DNA; (2) cells transformed by the vectors; (3) producing CC the fusion protein by culture of the transformed cells; (4) detecting CC hypoxic conditions in cells by monitoring the stability of the protein CC fused to (1) in cells transformed by vectors containing the DNA; (5) CC regulating the stability of proteins within the cell by transformation CC with the DNA; (6) inhibiting the development of cells under hypoxic CC conditions, using the fusion protein; (7) fusion proteins encoded by the CC DNA; and (8) stabilisation of cells under specific conditions of oxygen CC tension. (1) has cyostatic activity, and can be used for the

stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy; (II) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention

Sequence 49 BP; 15 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 26 GGAGCTAACATCTCCAAGTC 45

RESULT 4
ID ABZ71164/C
XX ABZ71164 standard / DNA; 54 BP.

XX 30-APR-2003 (first entry)

DS Hypoxia-inducible factor 1 alpha 557-574 peptide encoding DNA SEQ: 2.

XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;

KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;

XX tumour; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..54

FT /*tag= a

FT /partial

FT /product= "HIF-1 alpha 557-574 peptide"

FT /note= "no start or stop codons given"
XX WO200299104-A1.
XX PN 12-DEC-2002.
XX PP 04-JUN-2002; 2002WO-0P005432.
XX PR 05-JUN-2001; 2001JP-00169948.
XX PR 05-JUN-2001; 2001JP-00169949.
XX PA (POKK) POLA CHEM IND INC.
PA (HIRA) HIRAKA M.
PA (KOND) KOND OH S.
XX PI Hirao ka M, Kondoh S, Harada H;
XX DR WPI; 2003-148670/14.
DR P-PSDB; ABP57669.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX PS Claim 3; Page 58; 14pp; Japanese.

The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLMLAPITPMDDDFQL see ABP57669) (I), or encoding a fusion protein containing at least 16 residues of (I), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under hypoxic conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA, (2) cells transformed by the vectors, (3) producing the fusion protein by culture of the transformed cells; (4) detecting the fusion protein by culture of the transformed cells; (4) detecting the hypoxic conditions in cells by monitoring the stability of the protein

CC hypoxic conditions in cells by monitoring the stability of the protein fused to (I) in cells transfected by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (I) has cytostatic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (I) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence encodes (I) from the present invention

SQ Sequence 54 BP; 14 A; 11 C; 11 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 54 BP; 14 A; 11 C; 11 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cytostatic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (1) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention.

Sequence 57 BP; 15 A; 12 C; 13 G; 17 T; 0 U; 0 Other;

Query Match	100.0%	Score	20	DB	8	Length	57
Best Local Similarity	100.0%	Pred. No.	3.1				
Matches	20	Conservative	0	Mismatches	0	Gaps	0
Qy	1	GGAGCTAACATCTCCAAAGTC	20				
Db	28	GGAGCTAACATCTCCAAAGTC	9				

RESULT 6
ABZ76615 standard; DNA; 58 BP.
ID ABZ76615;

AC ABZ76615;

XX XX

30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:28.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic; hypoxic; solid tumour; gene therapy; microbial fermentation; medicine; tumour; nuclear localisation signal; oxygen dependent degradation domain; NLS; ODD; PCR primer; 88.

XX OS Homo sapiens.

XX PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK) POLA CHEM IND INC.

PA (HIRAKO /) HIRAKO M.

PA (KOND /) KONDOH S.

XX PI Hirakko M, Kondoh S, Harada H,

XX DR WPI; 2003-148670/14.

XX PS Example; Page 24; 144pp; Japanese.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to protein within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX PS Example; Page 23; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMAYIPMDDPQL see ABP5769) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein

fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cytostatic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (1) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention.

SQ Sequence 58 BP; 18 A; 13 C; 13 G; 14 T; 0 U; 0 Other;

Query Match	100.0%	Score	20	DB	8	Length	58
Best Local Similarity	100.0%	Pred. No.	3.1				
Matches	20	Conservative	0	Mismatches	0	Gaps	0
Qy	1	GGAGCTAACATCTCCAAAGTC	20				
Db	35	GGAGCTAACATCTCCAAAGTC	54				

RESULT 7
ABZ76607
ID ABZ76607 standard; DNA; 58 BP.

AC ABZ76607;

XX XX

30-APR-2003 (first entry)

DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:20.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic; hypoxic; solid tumour; gene therapy; microbial fermentation; medicine; tumour; nuclear localisation signal; oxygen dependent degradation domain; NLS; ODD; PCR primer; 88.

XX OS Homo sapiens.

XX PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK) POLA CHEM IND INC.

PA (HIRAKO /) HIRAKO M.

PA (KOND /) KONDOH S.

XX PI Hirakko M, Kondoh S, Harada H,

XX DR WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX Example; Page 23; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMAYIPMDDPQL see ABP5769) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein

fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cytotoxic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (1) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention

Sequence 58 BP; 19 A; 12 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTTACATCTCCAACTC 20
Db 35 GGAGCTTACATCTCCAACTC 54

RESULT 8

ABN3365/C
ID ABN3365 Standard; DNA; 60 BP.

XX
AC ABN33665;

XX
DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:6413.

XX Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.
OS Homo sapiens.
XX WO200210449-A2.
XX PN WO200299104-A1.
XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-1B001903.
XX PR 28-JUL-2000; 2000US-0221607P.
XX PR 02-MAY-2001; 2001US-0287724P.
XX PA (COMP-) COMGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Paigler S;
PI WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.
XX Example 1; SEQ ID NO 6413; 47bp; English.

CC The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-) transcriptome comprises messenger RNAs transcribed from multiple transcriptome units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue specific genes such as those genes only expressed in a specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice disorder. ABN2753 to ABN9589 represent Oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 BP; 16 A; 16 C; 10 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAACTC 20
Db 51 GGAGCTAACATCTCCAACTC 32

RESULT 9

ABZ71180/C
ID ABZ71180 standard; DNA; 66 BP.

XX AC ABZ71180;
XX DT 30-APR-2003 (first entry)

XX DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:19.
XX KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic; hypoxic; solid tumour; gene therapy; microbial fermentation; medicine; tumour; nuclear localisation signal; oxygen dependent degradation domain; NLS; ODD; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200299104-A1.
XX PR 04-JUN-2002; 2002WO-JP005482.
XX PR 05-JUN-2001; 2001JP-00168948.
XX PR 05-JUN-2001; 2001JP-0016949.
XX PA (POKK) POLA CHEM IND INC.
PA (HIRA/.) HIRAKA M.
PA (KOND/) KONDOH S.
XX PI Hirakawa M, Kondooh S, Harada H;
DR WPI; 2003-148670/14.

XX PT New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX PS Example; Page 23; 144pp; Japanese.
XX CC The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDPEMLAYIPMDDFQL see ABP57669) (1), or encoding a fusion protein containing at least 16 residues of (1) a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vector; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA; (5)

regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cytotoxic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (1) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention.

Sequence 66 BP; 17 A; 14 C; 14 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTTACATCTCCAGTC 20
Db 28 GGAGCTTACATCTCCAGTC 9

RESULT 10

ABZ76614/C
ID ABZ76614 standard; DNA; 66 BP.

XX AC ABZ76614;

XX DT 30-APR-2003 (first entry)

XX DE Human HIF-1 alpha ODD domain PCR primer SEQ ID NO:27.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; Stabilisation; cytotoxic;

KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;

KW tumour; nuclear localisation signal; oxygen dependent degradation domain;

KW NLS / ODD; PCR primer; SS.

XX Homo sapiens.

XX WO200299104-A1.

XX PD 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK) POLA CHEM IND INC.

PA (HIRAOKA M. (HIRAOKA M.

PA (KOND OH S. (KOND OH S.

XX PI Hirakawa M., Kondoh S., Harada H;

XX DR WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX Example; Page 24; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (IIDIEMIAPYIPDDDFQL see ABP57669) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation

CC regulating the stability of proteins within the cell by transformation with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension. (1) has cytotoxic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy. (1) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a PCR primer for the human HIF-1 alpha oxygen dependent degradation (ODD) domain, which is used in an example from the present invention.

SQ Sequence 66 BP; 16 A; 15 C; 15 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 66;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
Db 28 GGAGCTAACATCTCCAGTC 9

RESULT 11

ABZ71165/C
ID ABZ71165 standard; DNA; 168 BP.

XX AC ABZ71165;

XX DT 30-APR-2003 (first entry)

XX DE Nucleotide sequence SEQ ID NO:3.

XX Hypoxia-inducible factor 1 alpha; HIF-1 alpha; Stabilisation; cytotoxic; KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine; KW tumour; gene; ds.

XX Synthetic.

XX OS PN WO200299104-A1.

XX PD 12-DEC-2002.

XX PP 04-JUN-2002; 2002WO-JP005482.

XX PR 05-JUN-2001; 2001JP-00169948.

XX PR 05-JUN-2001; 2001JP-00169949.

XX PA (POKK) POLA CHEM IND INC.

PA (HIRAOKA M. (HIRAOKA M.

PA (KOND OH S. (KOND OH S.

XX PI Hirakawa M., Kondoh S., Harada H;

XX DR WPI; 2003-148670/14.

XX New DNA encoding a polypeptide imparting relative stability under hypoxic conditions to proteins within the cell, useful for treatment of cancer and improvement of microbial fermentation.

XX Disclosure; Page 59; 144pp; Japanese.

XX The present invention describes DNA encoding a hypoxia-inducible factor 1 alpha (HIF-1 alpha) amino acids 557 to 574 peptide (IIDIEMIAPYIPDDDFQL see ABP57669) (1), or encoding a fusion protein containing at least 16 residues of (1), a nuclear localisation signal (NLS), and another protein, and imparting relative stability under specific conditions of oxygen concentration within the cell. Also described: (1) vectors containing the DNA; (2) cells transformed by the vectors; (3) producing the fusion protein by culture of the transformed cells; (4) detecting hypoxic conditions in cells by monitoring the stability of the protein fused to (1) in cells transformed by vectors containing the DNA; (5) regulating the stability of proteins within the cell by transformation

with the DNA; (6) inhibiting the development of cells under hypoxic conditions, using the fusion protein; (7) fusion proteins encoded by the DNA; and (8) stabilisation of cells under specific conditions of oxygen tension; (I) has cytotoxic activity, and can be used for the stabilisation of a cytotoxic protein within cells in hypoxic regions of a solid tumour, and in gene therapy; (II) can be used in industrial microbial fermentation, and in medicine, especially in the treatment of tumours containing hypoxic regions. The present sequence represents a nucleotide sequence given in the exemplification of the present invention. N.B. The present sequence is given in the sequence listing of the present invention but is not mentioned further within the specification.

SQ Sequence 168 BP; 48 A; 44 C; 31 G; 45 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 168;
 Best Local Similarity 100.0%; Pred. No. 3, 5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAGCTAACATCCAAAGTC 20
 Db 50 GGAGCTAACATCTCAAGTC 31 ..

RESULT 12
 AAFA85323/C
 ID AAFA85323 standard; DNA; 1335 BP.
 XX

XX 23-JUL-2001 (first entry)

XX Nucleotide sequence of ttAK-hH104.

DE Nucleic acid construct; oxygen partial pressure; cellular hypoxia; KW anemia; cancer; ischemia; erythropoletin; immunotherapy;
 KW autoimmune disease; Hh104; TTAK; ss.
 XX Synthetic.
 OS XX

PH Key Location/Qualifiers
 PT CDS 1..1335
 PT /*tag= a
 XX WO200136616-A2.

XX PD 25-MAY-2001.
 XX PP 17-NOV-2000; 2000WO-FR003207.
 XX PR 18-NOV-1999; 99FR-00014513.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (AVET) AVENTIS PHARMA SA.

XX PI Beuzard Y, Payen E, Scherman D, Bettan M;
 XX DR WPI; 2001-343818/36.
 XX P-PSDB; AAB68415.

XX PT New nucleic acid construct for controlling expression of target gene, useful e.g. for treating cancer, is modulated by exogenous pharmaceutical and oxygen partial pressure.
 PT Disclosure; Page 55-57; 60pp; French.
 PS The specification describes a nucleic acid construct bearing a system for regulating the expression of a gene. The nucleic acid construct comprises at least one sequence encoding a protein that regulates expression of at least one gene of interest. The activity of this protein is modulated by presence/absence of a pharmacological agent and the amount of protein produced depends on the oxygen partial pressure. The constructs are used to treat conditions associated with cellular hypoxia, especially anemia,

CC cancer and ischemia, specifically where the gene of interest encodes erythropoletin (but many other suitable genes are listed, e.g. those encoding single-chain antibodies for immunotherapy of infections or autoimmune diseases, prodrug-converting enzymes, apoptosis inducers etc.). The present sequence represents the open reading frame of ttAK-hH104. The sequence contains a human hH104 fragment, inserted into the BstWI site of ttAK. The sequence is used to produce constructs of the invention.

XX SQ Sequence 1335 BP; 377 A; 323 C; 323 G; 312 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 1335;
 Best Local Similarity 100.0%; Pred. No. 4, 5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCAAGTC 20
 Db 749 GGAGCTAACATCTCAAGTC 730

RESULT 13

AEC31706/C
 ID AEC31706 standard; DNA; 1354 BP.

XX AC AEC31706;

XX DT 20-OCT-2005 (first entry)

XX DE Anoxia controlled transcription factor associated DNA, SEQ ID No:1.
 XX KW transcription factor; transcription; anoxia; gene expression; tumor; KW ischemia; heart disease; arthritis; cardiovascular-gen.; cytostatic; KW vasoconstrictor; cardiotonic; antiarthritic; ds.
 XX Unidentified.
 OS XX CN1580262-A.
 PN XX CN1580262-A.
 XX PD 16-FEB-2005.
 XX PP 12-AUG-2003; 2003CN-00142216.
 XX PR 12-AUG-2003; 2003CN-00142216.

XX PA (UYSH-) UNIV SHANGHAI NO 3 MEDICAL.

XX PI Ying LQG, Lu J;

XX DR WPI; 2005-372977/39.

XX PT Carrier system containing an artificial transcription factor regulated by oxygen deficit, and its configuration and use.
 XX Claim 2; SEQ ID NO 1; 27bp; Chinese.
 XX PS The invention relates to a transcription factor controlled by anoxia. The CC transcription factor is produced by a construction method in which GAL4 CC DNA combines and HIF1 is active. Also described is a carrier system CC containing the transcription factor of the invention. The system is CC composed of two carriers: (a) one carrier is controlled by anoxia and can activate targeted gene expression controlled by the G578A promoter, (b) CC the other carrier contains the G578A promoter. The invention allows the CC displacement of different promoters and the ability of controlling gene CC expression in cells and organisms undergoing anoxia. Different targeted CC genes can be coupled into the carrier for the preparation of therapeutic CC drugs for tumor, ischemia, angiocardiopathy and arthritis. This sequence CC represents DNA relating to the present invention.

XX SQ Sequence 1354 BP; 448 A; 267 C; 302 G; 337 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 14; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 4, 5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 773 GGAGCTAACATCTCCAAAGTC 754

RESULT 14
 ABV78154/C
 ID ABV78154 standard; DNA; 2481 BP.
 AC ABV78154;
 XX 15-NOV-2002 (first entry)
 DT Human HIF-alpha DNA SEQ ID NO 38.
 DB RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
 KW protozoacide; gene expression, antisense, tumour infection; Plasmodium;
 KW virus; viroid; anti- GFP; human; HIV; human immunodeficiency virus;
 KW Hepatitis C virus; human papilloma virus; gene; ds.
 OS Homo sapiens.
 XX OS Homo sapiens.
 PN DB1010588-A1.
 PD 18-JUL-2002.
 XX PR 09-JAN-2001; 2001DE-01000588.
 XX PR 09-JAN-2001; 2001DE-01000588.
 OS PR (RIBO-) RIBOPHARMA AG.
 XX PN WO20025693-A2.
 XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
 PD 18-JUL-2002.
 XX PR 09-JAN-2002; 2002WO-EP000152.
 XX PR 09-JAN-2001; 2001DB-01000586.
 XX PR 26-OCT-2001; 2001DB-01055280.
 XX PR 29-NOV-2001; 2001DB-01058411.
 XX PR 07-DEC-2001; 2001DE-01060151.
 XX PA (RIBO-) RIBOPHARMA AG.

Kreutzer R, Limmer S, Rost S, Hadwiger P;
 DR 2002-590671/63.

Inhibiting expression of target gene, useful e.g. for inhibiting
 PT oncogenes, by administering double-stranded RNA complementary to the
 target and having an overhang.
 PS Claim 10; Page 134-135; 203pp; German.

The invention relates to inhibiting expression of a target gene (I) in a
 CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
 CC structure of at most 49 consecutive bases. At least part of one strand
 CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
 CC in humans, also. Genes in Plasmodium or in viruses or viroids that are
 CC pathogenic for humans, animals or plants. Introducing an overhang into
 CC dsRNA greatly increases effectiveness for inhibiting gene expression,
 CC both in vivo and in vitro and also increases stability and thus the
 CC effective concentration inside the cell. The present sequence is that of
 CC a gene related to the invention.

SQ Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 2481;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1691 GGAGCTAACATCTCCAAAGTC 1672

RESULTS 15
 ABZ3530/C
 ID ABZ35730 standard; DNA; 2481 BP.
 XX ABZ35730;
 AC

Search completed: May 21, 2006, 21:17:45
 Job time : 262.5 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:16:50 ; Search time 2223.5 Seconds (without alignment)

502.985 Million cell. updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaggtaaacatctccaaatgc 20

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : EST:*

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1: gb_est1;*
2: gb_est3;*
3: gb_est4;*
4: gb_est5;*
5: gb_est6;*
6: gb_htc;*
7: gb_est7;*
8: gb_est8;*
9: gb_est9;*
10: gb_gbs1;*
11: gb_gbs1;*
12: gb_gbs2;*
13: gb_gbs3;*
14: gb_gbs4;*

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Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2	20 100.0	110	2 BF90491	BF90491 PM1-MT019
	2	20 100.0	165	2 BF734487	BF734487 PM2-AN008
C	3	20 100.0	222	10 T10413	T10413 hbc120 Huma
C	4	20 100.0	316	10 DY178075	DY178075 000407BTN
C	5	20 100.0	324	8 CN264306	CN264306 170005000
C	6	20 100.0	326	7 BE184816	BE184816 QV0-HF069
C	7	20 100.0	357	7 AW860308	AW860308 QV0-C7038
C	8	20 100.0	370	7 AW862545	AW862545 QV0-C7038
C	9	20 100.0	387	10 DY137624	DY137624 000127BLI
C	10	20 100.0	400	9 D5630	D5630 HUN428EB4B
C	11	20 100.0	421	7 AW00395	AW00395 MR2-AN006
C	12	20 100.0	421	7 BB69421	BB69421 QV0-C7038
C	13	20 100.0	424	7 DY048267	DY048267 000127BLI
C	14	20 100.0	445	7 BE695412	BE695412 QV0-C7038
C	15	20 100.0	453	11 AQ805950	AQ805950 HS_3125_A
C	16	20 100.0	454	7 BB69416	BB69416 QV0-C7038
C	17	20 100.0	464	3 BM835867	BM835867 K-BST0111
C	18	20 100.0	467	9 DA163304	DA163304 DA163304
C	19	20 100.0	470	11 AQ813482	AQ813482 HS_5269_A

ALIGNMENTS

RESULT 1
BF900491

LOCUS PM1-MT0198-061200-003-c05

DEFINITION MT0198 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF900491

VERSION 1

KEYWORDS GI:12291950

EST.

Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 110)

AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.J.R., Zago,M.A., Bordim,S., Costa,F.F., Goldstein,G.H., Carvalho,A.P., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and Simpson,A.J.

SEQUENCE tags Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBLISHER 10/37800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,
Brazil Tel: +55-11-27049322
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PDBSSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?tt=PM1&t2=PM1-MT0198-061200-003-c05&t4=1>

Seg primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 110
Location/Qualifiers 1.. 110
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="MT0198"
 /notes="Organ: narrow; vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match Score 100.0%; Score 20; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;

DEFINITION hbc120 Human pancreatic islet mRNA clone hbc120 5', end.

LOCUS T10413 mRNA
 hbc120 Human pancreatic islet Homo sapiens CDNA clone hbc120 5', end.
 mRNA sequence.

VERSION T10413
 KEYWORDS EST.

ACCESSION T10413.1
 GI:390567

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 222)
 Takeda, J., Yano, H., Eng, S., Zeng, Y. and Bell, G.I.: A molecular inventory of human pancreatic islets: sequence analysis of 1000 cDNA clones

AUTHORS Takeda, J.
 TITLE Hum. Mol. Genet. 2, 1793-1798 (1993)

JOURNAL T506601
 PUBLISHED Contact: Bell GI or Takeda J
 COMMENT HHMI
 Univ. of Chicago
 5841 S. Maryland Ave., MC1028, Chicago IL 60637
 Tel: 312/7329116
 Fax: 312/7320271
 Email: g-bell@uchicago.edu
 Seq primer: SK primer.
 Location/Qualifiers 1..222
 source /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="hbc120"

RESULT 3
 T10413/c

Query Match Score 100.0%; Score 20; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;

DEFINITION hbc120 Human pancreatic islet mRNA clone hbc120 5', end.

LOCUS T10413 mRNA
 hbc120 Human pancreatic islet Homo sapiens CDNA clone hbc120 5', end.
 mRNA sequence.

VERSION T10413.1
 GI:390567

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 222)
 Takeda, J., Yano, H., Eng, S., Zeng, Y. and Bell, G.I.: A molecular inventory of human pancreatic islets: sequence analysis of 1000 cDNA clones

AUTHORS Takeda, J.
 TITLE Hum. Mol. Genet. 2, 1793-1798 (1993)

JOURNAL T506601
 PUBLISHED Contact: Bell GI or Takeda J
 COMMENT HHMI
 Univ. of Chicago
 5841 S. Maryland Ave., MC1028, Chicago IL 60637
 Tel: 312/7329116
 Fax: 312/7320271
 Email: g-bell@uchicago.edu
 Seq primer: SK primer.
 Location/Qualifiers 1..222
 source /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="hbc120"

RESULT 2
 BF734487

Query Match Score 100.0%; Score 20; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;

DEFINITION PM2-AN0089-081100-011-e04 AN0089 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF734487

VERSION BF734487.1
 GI:12059724

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 165)

REF ID: Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silveira, W.Jr., Zagó, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsumura, A., Baita, G.S., Simpson, D.H., Brunstein, A., Soeiro, P.S., Bucher, P., Jongenssen, C.V., Oliveira, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBLMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/Scripts/Bscripts/Gethm12.Pr?t1=PM2&t2=PM2-AN0089-081100-011-e04&t3=2000-11-08&t4=1>)

Seq primer: PUC 18 forward
 High quality sequence start: 20
 High quality sequence stop: 164.

Location/Qualifiers 1..165
 source /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="AN0089"

RESULT 4
 DY178075/c

Query Match Score 100.0%; Score 20; DB 10; Length 222;
 Best Local Similarity 100.0%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;

DEFINITION 000407BTNA005141HT BTNA Bos taurus cDNA, mRNA sequence.

LOCUS DY178075 mRNA
 BTNA Bos taurus cDNA, mRNA sequence.

VERSION DY178075.1
 EST.

KEYWORDS Bos taurus (cattle)

SOURCE Organism

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthari; Laurasiatheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae; Bovinae; Bos.

DEFINITION 000407BTNA005141HT BTNA Bos taurus cDNA, mRNA sequence.

LOCUS DY178075 mRNA
 BTNA Bos taurus cDNA, mRNA sequence.

VERSION DY178075.1
 EST.

KEYWORDS Bos taurus (cattle)

SOURCE Organism

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthari; Laurasiatheria; Cetartiodactyla; Ruminantia;

REFERENCE	1 (bases 1 to 316)	ORIGIN	/note="Oligo dT primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"
AUTHORS	McCulloch, A., Wilson, T., Molenaar, A., Grigor, M., Davis, S., Glenn, M., Havukkala, I., Watson, J., Crawford, A., Wheeler, T., Fagreman, L., Lee, R., Hein, W., Johnstone, P., Maqbool, N., McMahon, C., McCracken, J., Strelwagen, K., Farr, V., Singh, K., Whitley, J., Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J., Wells, M., Bowman, P., Goddard, M., Langford, C., McEvans, J. and Atkinson, P.	FEATURES	Query Match 100.0%; Score 20; DB 8; Length 324; Best Local Similarity 100.0%; Pred. No. 32; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TITLE	Unpublished	COMMENT	AGResearch, Genesis and Primary Industry Victoria Bovine EST Project
JOURNAL	Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand	FEATURES	RESULT 6 BEI84816 LOCUS BB184816 mRNA linear EST 22-JUN-2000 DEFINITION QV4-HT0691-270400-186-g04 HT0691 Homo sapiens cDNA, mRNA sequence. ACCESSION BEI84816 VERSION BEI84816.1 GI:8664000 KEYWORDS EST. ORGANISM Homo sapiens (human) Mammalia: Eutheria: Euarchontoglires: Primates: Catarrhini: Hominoidea: Homo: Hominidae: Homo REFERENCE 1 (bases 1 to 326) AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W.J.R., Zago, M.A., Bordim, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukawa, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J. TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-27049222 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV4-HT0691-2704-186-g04&t3=2000-04-27&t4=1) Seq. Primer: puc 18 forward High quality sequence start: 9 High quality sequence stop: 326. Location/Qualifiers 1..326 FEATURES /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="HT0691" /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES	Query Match 100.0%; Score 20; DB 7; Length 326; Best Local Similarity 100.0%; Pred. No. 32; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
COMMENT	1 GGAGCTAACATCTCCAACTC 20 Db 78 GGAGCTAACATCTCCAACTC 59		
FEATURES	RESULT 5 CN264306/C LOCUS CN264306 mRNA linear EST 16-MAY-2004 DEFINITION 17000600020922 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence. ACCESSION CN264306 VERSION CN264306.1 KEYWORDS EST. ORGANISM Homo sapiens (human) Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Euarchontoglires: Primates: Catarrhini: Hominoidea: Homo REFERENCE 1 (bases 1 to 324) AUTHORS Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Leibowski, J. and Stanton, L.W. TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004) COMMENT Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 324 Std Error: 0.00. Location/Qualifiers 1..324 FEATURES /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cells, DMSO-treated H9 cell line" /clone_lib="GRN_PREHEP"		
FEATURES	Query Match 100.0%; Score 20; DB 7; Length 326; Best Local Similarity 100.0%; Pred. No. 32; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
COMMENT	1 GGAGCTAACATCTCCAACTC 20		

Db	262	GGAGCTAACATCTCCAGTC 281	KEYWORDS EST. Homo sapiens (human)	ORGANISM Homo sapiens
RESULT	7			
AV860808	AV860808	AW860808 mRNA linear EST 19-MAY-2000		
LOCUS	QVO-CT0383-210400-206-h08	357 bp CT0383 Homo sapiens CDNA, mRNA sequence.		
DEFINITION	QVO-CT0383-210400-206-h08			
ACCESSION	AW860808			
VERSION	AW860808.1	GI:7956410		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 370)		
REFERENCE	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.			
AUTHORS		Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
TITLE		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
JOURNAL				
PUBLISHED	10/7/800			
COMMENT		Contact: Simpson A.J.G.		
Laboratory of Cancer Genetics		Ludwig Institute for Cancer Research		
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil				
TELEPHONE	+55-11-2704922			
FAX	+55-11-2707001			
EMAIL	asimpson@ludwig.org.br	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QVO-CT0383-210400-206-d12&t3=200-04-21&t4=1)		
SEQ PRIMER	Puc 18 forward	Seq primer: Puc 18 forward		
HIGH QUALITY SEQUENCE START	18	High quality sequence start: 18		
HIGH QUALITY SEQUENCE STOP	368	High quality sequence stop: 368.		
LOCATION/QUALIFIERS		Location/Qualifiers 1. 370		
FEATURES		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"		
Source		/dev_stages="Adult" /clone_lib="CT0383"		
		/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
ORIGIN		Query Match 100 0%; Score 20; DB 7; Length 370;		
		Best Local Similarity 100 0%; Pred. No. 33; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gapsp 0;		
		DEFINITION 000127BLIB006163HT BLIB Bos taurus cDNA, mRNA sequence.		
		ACCESSION DY137624		
		VERSION D137624.1		
		KEYWORDS EST.		
		ORGANISM Bos taurus (cattle)		
RESULT	9			
Qy	1	GGAGCTAACATCTCCAGTC 20	DY137624/C	
Db	19	GGAGCTAACATCTCCAGTC 38	387 bp mRNA linear EST 01-FEB-2006	
ORIGIN				
RESULT	9			
Qy	1	GGAGCTAACATCTCCAGTC 20	DY137624	
Db	19	GGAGCTAACATCTCCAGTC 38	370 bp mRNA linear EST 19-MAY-2000	
ORIGIN				
RESULT	8			
AWB62545	AWB62545	AWB62545 mRNA linear EST 19-MAY-2000		
LOCUS	OVO-CT0383-210400-206-d12	370 bp CT0383 Homo sapiens CDNA, mRNA sequence.		
DEFINITION	OVO-CT0383-210400-206-d12			
ACCESSION	AWB62545			
VERSION	AWB62545.1	GI:7958243		
REFERENCE	1 (bases 1 to 387)			
AUTHORS	McCulloch, A., Wilson, T., Molenaar, A., Grigor, M., Davis, S., Glenn, M., Havukkala, I., Watson, J., Crawford, A., Wheeler, T., Hagemann, L., Lee, R., Hein, W., Johnstone, P., Magbolo, N., McMahon, C.,			

McCracken,J., Stelwagen,K., Parr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and Atkinson,J.	Qy 1 GGAGCTAACATCTCCAGTC 20 Db 193 GGAGCTAACATCTCCAGTC 174
TITLE AgResearch, Genesis and Primary Industry Victoria Bovine EST Project	
JOURNAL Unpublished (2006)	RESULT 11
COMMENT Contact: Magpool N	Qy AW800395/c
AgResearch Ltd	LOCUS AW800395
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,	DEFINITION MR2-UM061-050400-105-a08
Mosgiel, New Zealand	VERSION UN0061 Homo sapiens cDNA, mRNA sequence.
Email: nauman.magpool@agresearch.co.nz.	KEYWORD EST
FEATURES	ORGANISM Homo sapiens (human)
source	Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;
REFERENCE	1 (bases 1 to 421) Dias,Nego,E., Garcia,Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordim,S., Costa,P.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and Simpson,A.J.
AUTHORS	Shortgun sequencing of the human transcriptome with ORF expressed sequence tags
ORIGIN	TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Query Match	JOURNAL JOURNAL OF CLONAL GENETICS
Best Local Similarity 100.0%; Pred. No. 34;	PUBMED 10737800
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001
ORIGIN	REFERENCE Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tt=&t=2-MR2-UM0061-050 400-105-a08&t3=2000-04-05&t4=1) KEYWORD Seq. primer: puc 18 forward High quality sequence start: 20 High quality sequence stop: 420. FEATURES source 1..421 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_idb="UM0061" /note="Organ: uterus; Vector: puc18; Site_1: Small; Site_2: Small; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
RESULT 10	ORIGIN
LOCUS D56430	Query Match 100.0%; Score 20; DB 7; Length 421;
DEFINITION HUM28EB04B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-428EB04 5', mRNA sequence.	Best Local Similarity 100.0%; Pred. No. 34;
ACCESSION D56430	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagatani,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomura,H., Takaichi,O., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.	
TITLE	
JOURNAL	
Unpublished (1995)	
COMMENT	
Contact: Tsutomu Fujiwara	
Osuka GEN Research Institute	
Otsuka Pharmaceutical Co.,Ltd	
463-10 KagaBunko Kawauchi-cho, Tokushima, 771-01 Japan	
Tel: 0886-6-3888	
Fax: 0886-37-1035.	
FEATURES	Location/Qualifiers
source	1..400
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	/mol_type="mRNA"
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	/clone_lib="Clontech human fetal brain polyA+ mRNA (#6535)"
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Best Local Similarity 100.0%; Pred. No. 34;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 12	
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LOCUS BE696421	Db 278 GGAGCTAACATCTCCAGTC 259
DEFINITION QV0-C0383-300600-290-h02 CT0383 Homo sapiens cDNA, mRNA sequence.	ACCESSION BE696421

VERSION KEYWORDS SOURCE ORGANISM	BB696421.1 EST. Homo sapiens (human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Gi:1:0083581 TITLE COMMENT	Hagemann,L., Lee,R., Hein,W., Johnstone,P., Macpool,N., McMahon,C., McCracken,J., Stevagen,K., Farr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and Atkinson,P. Agresearch, Genesis and Primary Industry Victoria Bovine EST project Unpublished (2006) Contact: Macpool N AgResearch Ltd. Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mogiel, New Zealand Email: rauhan.macpool@agresearch.co.nz.
REFERENCE AUTHORS	1. (bases 1 to 421) Dias Neto,F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Naga,M.A., da Silva,W.Jr., Costa,P.F., Goldman,M.A., Bordin,S., Simpson,D.H., Brunstein,A., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,C.V., O'Hare,M.J., Soares,F., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., Simpson,A.J.	JOURNAL COMMENT	Shotgun sequencing of the human transcriptome with ORF expressed sequence tag Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
TITLE JOURNAL PUBMED COMMENT	Sequence tag Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	FEATURES source	1. .421 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="Liver" /clone_id="BLIB" /note="Vector: PBK-CMV; Bovine liver cDNA library 'B' derived from tissue harvested from an unknown breed calf by Allan Crawford on 28/09/95"
ORIGIN	Query Match Best Local Similarity Matches Qy Db	Query Match Best Local Similarity Matches Qy Db	100.0%; Score 20; DB 10; Length 424; 100.0%; Score 100; DB 34; Pred. No. 34; 20; Conservative; 0; Mismatches 0; Indels 0; Gaps 0; 1 GGAGCTAACATCTCCAGTC 20 244 GGAGCTAACATCTCCAGTC 225
RESULT LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BB696412 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 14 BE696412 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match Best Local Similarity Matches Qy Db
COMMENT	1. .421 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="CT0383" /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORETES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	1. (bases 1 to 445) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Naga,M.A., da Silva,W.Jr., Zato,M.A., Bordin,S., Costa,F.F., Goldman,M.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	10/37800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAESP/LICR Human Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?l1=&l2=QV0-CT0383-300 600-290-e05ct3=200-00-30ct4-1) Seq primer: puc 18 forward High quality sequence start: 29 High quality sequence stop: 445. Location/Qualifiers
ORIGIN	DY048267/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 13 DY048267/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match Best Local Similarity Matches Qy Db
COMMENT	1. (bases 1 to 424) McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S., Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.	Query Match Best Local Similarity Matches Qy Db	100.0%; Score 20; DB 7; Length 421; 100.0%; Score 100; DB 34; Pred. No. 34; 20; Conservative; 0; Mismatches 0; Indels 0; Gaps 0; 1 GGAGCTAACATCTCCAGTC 20 18 GGAGCTAACATCTCCAGTC 37

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CT0383"
 /note="Organ: colon; Vector: pUC18; Site 1: Smal; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the PUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Query Match Similarity 100.0%; Score 20; DB 7; Length 445;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Qy 1 ||||| ||||| ||||| |||||
 Db 33 GGAGCTAACATCCAACTC 52

RESULT 15
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 LOCUS AQB05950 453 bp linear GSS 09-AUG-1999
 DEFINITION Human Genomic clone Plate=3025 Col=6 Row=E, genomic survey
 Sequence.
 Bacteria; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo;
 1 (bases 1 to 453)
 REFERENCES 1
 AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swarzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hod L.
 TITLE Sequencing-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10439764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 516-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3025; row: E; column: 6
 Seq primer: M13 Reverse
 Class: BAC ends
 High Quality sequence STOP: 453.
 Location/Qualifiers
 1..453
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 /mol_type="Genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3025 Col=6 Row=E"
 /sex="male"
 /clone_lib="CT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones In
 E-Coli DH10B"

ORIGIN
 Query Match Similarity 100.0%; Score 20; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 35;

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Om nucleic - nucleic search, using bw model.

Run on: May 21, 2006, 21:18:10 ; Search time 79.5 Seconds (without alignments)

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggaggtaaacatctccaaatgc 20

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1403665 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6A COMB .seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6B COMB .seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7 COMB .seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H COMB .seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/PCUTUS COMB .seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	20	100.0	2517	3 US-09-967-388-3	Sequence 3, Appli
c 2	20	100.0	2770	3 US-09-949-016-1518	Sequence 1518, Appli
c 3	20	100.0	3229	3 US-09-919-039-1448	Sequence 148, Appli
c 4	20	100.0	3678	3 US-09-930-662-22	Sequence 22, Appli
c 5	20	100.0	3678	3 US-09-939-873B-19	Sequence 19, Appli
c 6	20	100.0	3678	3 US-10-028-158-22	Sequence 22, Appli
c 7	20	100.0	3736	2 US-08-480-473B-1	Sequence 1, Appli
c 8	20	100.0	3736	3 US-08-945-213B-1	Sequence 1, Appli
c 9	20	100.0	3736	3 US-09-949-547-1	Sequence 1, Appli
c 10	20	100.0	3736	3 US-09-235-217-1	Sequence 1, Appli
c 11	20	100.0	3736	3 US-09-363-581-1	Sequence 1, Appli
c 12	20	100.0	3736	7 PCR-US96-1-0251-1	Sequence 1, Appli
c 13	20	100.0	3933	3 US-09-949-016-13218	Sequence 218, Appli
c 14	20	100.0	18120	3 US-09-949-016-13260	Sequence 13260, Appli
c 15	20	100.0	56714	3 US-09-949-016-11960	Sequence 11960, Appli
c 16	18.4	92.0	2481	3 US-10-010-81-1	Sequence 1, Appli
c 17	16.8	84.0	96	2 US-07-648-798A-22	Sequence 22, Appli
c 18	16.8	84.0	393	2 US-07-648-798A-12	Sequence 12, Appli
c 19	16.8	84.0	600	3 US-09-935-98-258	Sequence 258, Appli
c 20	16.8	84.0	1131	2 US-07-648-798A-14	Sequence 14, Appli
c 21	16.8	84.0	2313	2 US-07-648-798A-16	Sequence 16, Appli
c 22	16.8	84.0	2400	2 US-07-648-798A-15	Sequence 15, Appli
c 23	16.8	84.0	10697	3 US-09-949-016-13112	Sequence 13112, Appli

RESULT 1

US-09-967-388-3/c

; Sequence 3, Application US/09967388

; Patent No. 6818430

; GENERAL INFORMATION:

; APPLICANT: JEFFREY M. ARBEIT

; TITLE OF INVENTION: USE OF HIF-ALPHA VARIANTS TO ACCELERATE

; FILE REFERENCE: UC077-001A

; CURRENT APPLICATION NUMBER: US/09/967-388

; CURRENT FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2517

; TYPE: DNA

; ORGANISM: HUMAN

US-09-967-388-3

ALIGNMENTS

Query Match 100.0%; Score 20; DB 3; Length 2517;

Best Local Matches 20;	Similarity Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy 1 GGAGCTAACATCTCCAGTC 20

Db 1727 GGAGCTAACATCTCCAGTC 1708

RESULT 2

US-09-949-016-1518/c

; Sequence 1518, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949_016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-00

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 1518
; LENGTH: 2770
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1518

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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 811 GGAGCTAACATCTCCAAAGTC 792

RESULT 5
US-09-959-873B-19/c
; Sequence 19, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; ATTORNEY: Maxwell, Patrick Henry
; PUGET, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; ASSAY Factor, and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 1547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; CURRENT FILING DATE: 2001-11-09
; PRIOR FILING DATE: 2000-05-12
; PRIORITY NUMBER: GB9911047.0
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-959-873B-19

Query Match 100.0%; Score 20; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
Db 1719 GGAGCTAACATCTCCAAAGTC 1700

RESULT 6
US-10-028-158-22/c
; Sequence 22, Application US/10028158
; Patent No. 6863880
; GENERAL INFORMATION:
; APPLICANT: Canisgia, Isabella
; ATTORNEY: Post, Martin
; PUGET, Stephen
; TITLE OF INVENTION: MBTHOPS TO DIAGNOSE A REQUIRED REGULATION OF
; TROPHOBlast
; FILE REFERENCE: 11757.380SWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1999-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: 
; NAME/KEY: CDS
; LOCATION: (29)..(2509)
; NAME/KEY: CDS
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LOCATION: (29) .. (2509)
 US-10-028-158-22

Query Match Score 20; DB 3; Length 3678;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1719 GGAGCTAACATCTCCAAAGTC 1700

RESULT 7
 US-08-480-473B-1/c
 Sequence 1, Application US/08480473B
 Patent No. 5882914

GENERAL INFORMATION:
 APPLICANT: Semenza, Gregg L.
 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,473B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Halle, Lisa A.
 REGISTRATION NUMBER: 38 347

REFERENCE/DOCKET NUMBER: 07265/053001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/677-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3736 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

US-08-480-473B-1

Query Match Score 20; DB 2; Length 3736;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAACTC 20
 Db 1719 GGAGCTAACATCTCCAACTC 1700

RESULT 8
 US-08-915-213-1/c
 Sequence 1, Application US/08915213
 Patent No. 6030462

GENERAL INFORMATION:
 APPLICANT: Semenza, Gregg L.
 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla

US-09-148-547-1/c
 Sequence 1, Application US/09148547
 Patent No. 6124131

GENERAL INFORMATION:
 APPLICANT: Semenza, Gregg L.
 TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
 FILE REFERENCE: 07265/151001
 CURRENT APPLICATION NUMBER: US/09/148,547
 CURRENT FILING DATE: 1998-08-25
 NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3736
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (29) .. (2509)

US-09-148-547-1

Query Match Score 20; DB 3; Length 3736;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1719 GGAGCTAACATCTCCAACTC 1700

RESULT 10
 US-09-235-217-1/c
 Sequence 1, Application US/09235217

Patent No. 6222018
 GENERAL INFORMATION:
 APPLICANT: Semenza, Gregg L.
 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/235,217
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/480,473
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Liba A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07255/053001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3736 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-235-17-1

Query Match 100.0%; Score 20; DB 3; Length 3736;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
 Db 1719 GGAGCTAACATCTCCAGTC 1700

RESULT 12
 PCT-US96-10251-1/c
 Sequence 1, Application PC/TUS9610251
 GENERAL INFORMATION:
 APPLICANT: The Johns Hopkins University School of Medicine
 TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10251
 FILING DATE: 06-JUN-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Liba A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/053W01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3736 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 PCT-US96-10251-1

Query Match 100.0%; Score 20; DB 7; Length 3736;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAGTC 20
 Db 1719 GGAGCTAACATCTCCAGTC 1700

RESULT 13
 US-09-949-016-218/c
 Sequence 218, Application US/0949016
 GENERAL INFORMATION:
 APPLICANT: Venter, J. Craig et al.
 TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
 NUMBER OF SEQ ID NOS: 2
 FILE REFERENCE: JHU1500-1
 CURRENT APPLICATION NUMBER: US/09/383,581
 CURRENT FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/148,547
 PRIOR FILING DATE: 1998-08-25
 SEQ ID NO 1
 LENGTH: 3736
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: CDS
 LOCATION: (29)...(2509)
 US-09-383-581-1

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 218
; LENGTH: 3933
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-218

Query Match          100.0%; Score 20; DB 3; Length 56714;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1955 GGAGCTAACATCTCCAAAGTC 1936

Search completed: May 21, 2006, 21:20:58
Job time : 82.5 secs

RESULT 14
US-09-949-016-13260/C
; Sequence 13260, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13260
; LENGTH: 18120
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13260

Query Match          100.0%; Score 20; DB 3; Length 18120;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGCTAACATCTCCAAAGTC 20
Db      8653 GGAGCTAACATCTCCAAAGTC 8634

RESULT 15
US-09-949-016-11960/C
; Sequence 11960, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11960
; LENGTH: 56714

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:21:21 ; Search time 823 Seconds

(without alignments)
298.606 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggacctaacatctccaaatgc 20

Scoring table: IDENTITY_NUC

GapOp 10.0 , GapExt 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications NA_Main:*

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3: /EMC_Celerra_SIDS3/podata/2/pubnpna/US09_PUBCOMB.seq;*
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11: /EMC_Celerra_SIDS3/podata/2/pubnpna/US10F_PUBCOMB.seq;*
12: /EMC_Celerra_SIDS3/podata/2/pubnpna/US10G_PUBCOMB.seq;*
13: /EMC_Celerra_SIDS3/podata/2/pubnpna/US11A_PUBCOMB.seq;*
14: /EMC_Celerra_SIDS3/podata/2/pubnpna/US11B_PUBCOMB.seq;*
15: /EMC_Celerra_SIDS3/podata/2/pubnpna/US11C_PUBCOMB.seq;*
16: /EMC_Celerra_SIDS3/podata/2/pubnpna/US11D_PUBCOMB.seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	20	100.0	20	8 US-10-766-185-3	Sequence 3, Appli
c 2	20	100.0	20	8 US-10-766-185-3	Sequence 4, Appli
c 3	20	100.0	60	3 US-09-908-975-6413	Sequence 541, Appli
c 4	20	100.0	2481	8 US-10-384-339C-38	Sequence 3, Appli
c 5	20	100.0	2481	8 US-10-384-339C-38	Sequence 38, Appli
c 6	20	100.0	2487	10 US-10-450-163-20859	Sequence 20859, Appli
c 7	20	100.0	2517	3 US-09-967-388-3	Sequence 3, Appli
c 8	20	100.0	2528	7 US-10-204-724-2	Sequence 2, Appli
c 9	20	100.0	2861	7 US-10-264-449-431	Sequence 431, Appli
c 10	20	100.0	3180	7 US-10-425-584-3	Sequence 3, Appli
c 11	20	100.0	3229	3 US-09-919-139-148	Sequence 148, Appli
c 12	20	100.0	3229	6 US-10-208-108-22	Sequence 22, Appli
c 13	20	100.0	3229	6 US-10-084-817-113	Sequence 113, Appli
c 14	20	100.0	3229	7 US-10-247-671-19	Sequence 19, Appli
c 15	20	100.0	3551	8 US-10-304-126-13	Sequence 13, Appli
c 16	20	100.0	3551	9 US-10-719-370A-13	Sequence 22, Appli
c 17	20	100.0	3678	6 US-10-028-158-22	Sequence 1, Appli

C	18	20	100.0	3678	9 US-10-901-583-19
c 19	20	100.0	3678	10 US-10-007-255-3	
c 20	20	100.0	3678	13 US-11-043-493-22	
c 21	20	100.0	3736	10 US-10-831-380-1	
c 22	20	100.0	3736	9 US-10-699-557-3	
c 23	20	100.0	3812	9 US-10-172-118-625	
c 24	20	100.0	3927	3 US-10-383-790-231	
c 25	20	100.0	3933	7 US-10-388-360-309	
c 26	20	100.0	3933	7 US-10-388-360-309	
c 27	20	100.0	3933	8 US-10-342-387-625	
c 28	20	100.0	3933	8 US-10-407-807-1	
c 29	20	100.0	3933	8 US-10-304-116-4	
c 30	20	100.0	3933	9 US-10-719-370A-4	
c 31	20	100.0	3933	9 US-10-719-370A-133	
c 32	20	100.0	3933	9 US-10-848-646-3	
c 33	20	100.0	3933	10 US-10-956-157-643	
c 34	20	100.0	3933	10 US-10-494-800-59	
c 35	20	100.0	3933	16 US-11-288-720-1	
c 36	20	100.0	3958	9 US-10-699-557-2	
c 37	20	100.0	4162	10 US-10-450-763-20862	
c 38	20	100.0	4156	6 US-10-044-090-284	
c 39	20	100.0	4227	7 US-10-115-987-12	
c 40	20	100.0	4740	7 US-10-115-987B-13	
c 41	20	100.0	10355	7 US-10-204-724-4	
c 42	20	100.0	57501	9 US-10-719-370A-11	
c 43	20	100.0	57501	8 US-10-304-126-11	
c 44	18.4	92.0	2481	6 US-10-001-846-1	
c 45	18.4	92.0	2481	9 US-10-854-483-1	

ALIGNMENTS

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RESULT 1
US-10-766-185-3/c
; Sequence 3, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-10-766-185-3
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Query Match	Best Local Similarity	Score 20;	DB 8;	Length 20;
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 GGAGCTAACATCTCCAGTC 20			
Db	20 GGAGCTAACATCTCCAGTC 1			

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RESULT 2
US-10-766-185-4
; Sequence 4, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-10-766-185-4
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APPLICANT: Jiang, Xiaoming
 TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
 FILE REFERENCE: REX 7034
 CURRENT APPLICATION NUMBER: US/10/766,185
 CURRENT FILING DATE: 2004-01-28
 NUMBER OF SEQ ID NOS: 130
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 4
 LENGTH: 20
 TYPE: DNA
 ORGANISM: artificial sequence
 OTHER INFORMATION: antisense oligonucleotide
 US-10-766-185-4

Query Match Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.4%;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATTCGAAGTC 20
 Db 1 GGAGCTAACATTCGAAGTC 20

RESULT 4
 US-09-908-975-6413/c
 Sequence 6413, Application US/09908975
 Publication No. US20030165843A1
 GENERAL INFORMATION:
 APPLICANT: SHOSHAN, Avi
 APPLICANT: WASSERMAN, Alon
 APPLICANT: MINTZ, Liat
 APPLICANT: FAIGLER, Shimchon
 TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
 TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
 FILE REFERENCE: 36688-0005
 CURRENT FILING DATE: 2001-07-20
 PRIOR APPLICATION NUMBER: US/09/908,975
 PRIOR FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: US 60/221,607
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 3237
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 6413
 LENGTH: 60
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-908-975-6413

Query Match Score 20; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.9%;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATTCGAAGTC 20
 Db 51 GGAGCTAACATTCGAAGTC 32

RESULT 5
 US-10-384-339C-38/c
 Sequence 38, Application US/10384339C
 Publication No. US20040175703A1
 GENERAL INFORMATION:
 APPLICANT: Kreuzer, Roland
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET
 FILE REFERENCE: 20200/2002
 CURRENT APPLICATION NUMBER: US/10/384,339C
 PRIOR APPLICATION NUMBER: PCT/EP02/00152
 PRIOR FILING DATE: 2002-03-07
 PRIOR APPLICATION NUMBER: PCT/EP02/00152
 PRIOR FILING DATE: 2002-01-09
 PRIOR APPLICATION NUMBER: DE 10100566.5
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: DE 10155280.7
 PRIOR FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: DE 10158411.3
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: DE 10160151.4
 PRIOR FILING DATE: 2001-12-07
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 38
 LENGTH: 2481
 TYPE: DNA
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 TITLE: Hif-alpha
 PATENT DOCUMENT NUMBER: U22431

US-10-384-339C-38

Query Match Score 20; DB 8; Length 2481;
 Best Local Similarity 100.0%; Pred. No. 7.3%;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATTCGAAGTC 20
 Db 1691 GGAGCTAACATTCGAAGTC 1672

RESULT 6
 US-10-15-763-20859/c
 Sequence 20859, Application US/10450763
 Publication No. US20050196754A1
 GENERAL INFORMATION:
 APPLICANT: HYSEQ, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 FILE REFERENCE: 790C1P3/US
 CURRENT APPLICATION NUMBER: US/10/450,763
 CURRENT FILING DATE: 2003-06-11
 PRIOR APPLICATION NUMBER: PCT/US01/08631

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; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 20859
; LENGTH: 2487
; TYPE: DNA
; FEATURES:
;   /organism: Homo sapiens
;   /name/key: SIMILAR
;   /location: (574) .(2487)
; OTHER INFORMATION: 99% homologous to Homo sapiens 06-JUN-1995 Human hypoxia
; OTHER INFORMATION: Inducible factor-1 alpha cDNA, accession number T4533_2cl, Smith-
US-10-450-763-20859

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 2487;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 1697 GGAGCTAACATCTCCAAGTC 1678

RESULT 7
US-09-967-388-3/c
; Sequence 3, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
;   APPLICANT: JEFFERERY M. ARBETT
;   TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
;   FILE REFERENCE: UC077 001A
;   CURRENT APPLICATION NUMBER: US/09/967,388
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 3
;   LENGTH: 2517
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-967-388-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2517;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 1727 GGAGCTAACATCTCCAAGTC 1708

RESULT 8
US-10-204-724-2/c
; Sequence 2, Application US/10204724
; GENERAL INFORMATION:
;   APPLICANT: Kingman, John Alan
;   TITLE OF INVENTION: DIFFERENTIAL EXPRESSION SCREENING METHOD
;   FILE REFERENCE: 5326820000200
;   CURRENT APPLICATION NUMBER: US/10/204,724
;   CURRENT FILING DATE: 2002-08-21
;   PRIOR APPLICATION NUMBER: PCT/GB01/00758
;   PRIOR FILING DATE: 2001-02-22
;   PRIOR APPLICATION NUMBER: GB 0018679.1
;   PRIOR FILING DATE: 2000-07-28
;   PRIOR APPLICATION NUMBER: GB 00041197.0
;   NUMBER OF SEQ ID NOS: 16

Query Match
Best Local Similarity 100.0%; Score 20; DB 7; Length 2528;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 1718 GGAGCTAACATCTCCAAGTC 1699

RESULT 9
US-10-264-049-431/c
; Sequence 431, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
;   APPLICANT: Birbe et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;   FILE REFERENCE: PAJ3P1
;   CURRENT APPLICATION NUMBER: US/10/264,049
;   CURRENT FILING DATE: 2002-10-04
;   PRIOR APPLICATION NUMBER: PCT/US01/18569
;   PRIOR FILING DATE: 2001-06-07
;   PRIOR APPLICATION NUMBER: US 60/209,467
;   PRIOR FILING DATE: 2000-06-07
;   SOFTWARE: PatentIn Ver. 3.1
;   SEQ ID NO 431
;   LENGTH: 2851
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2853)..(2853)
;   NUMBER OF SEQ ID NOS: 4360
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-431

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 841 GGAGCTAACATCTCCAAGTC 822

RESULT 10
US-10-425-784-3/c
; Sequence 3, Application US/10425784
; Publication No. US2004009591A1
; GENERAL INFORMATION:
;   APPLICANT: Hoffmann, Michael
;   APPLICANT: Allen-Hoffmann, Lynn
;   APPLICANT: Comer, Allen
;   TITLE OF INVENTION: Keratinocytes Expressing Exogenous Angiogenic Growth
;   FILE REFERENCE: STRATA 08110
;   CURRENT APPLICATION NUMBER: US/10/425,784
;   CURRENT FILING DATE: 2003-04-29
;   PRIOR APPLICATION NUMBER: 60/376,488
;   PRIOR FILING DATE: 2002-04-30
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 3
;   LENGTH: 3180
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-425-784-3

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Query Match 100.0%; Score 20; DB 7; Length 3180;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1955 GGAGCTAACATCTCCAAAGTC 1936

RESULT 11
 US-09-9-19-039-148/c
 ; Sequence 148, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIORITY NUMBER: 60/222,113
 ; PRIORITY FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 148
 ; LENGTH: 3229
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc feature
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CB1
 US-09-9-19-039-148

Query Match 100.0%; Score 20; DB 3; Length 3229;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1958 GGAGCTAACATCTCCAAAGTC 1939

RESULT 12
 US-10-208-408-22/c
 ; Sequence 22, Application US/10208408
 ; Publication No. US20030096272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schepke, Xiao Min
 ; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
 ; FILE REFERENCE: PA-0048-1 US
 ; CURRENT APPLICATION NUMBER: US/10/208,408
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIORITY NUMBER: 60/308,868
 ; PRIORITY FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 22
 ; LENGTH: 3229
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030096272A1 1250434CB1
 US-10-208-408-22

Query Match 100.0%; Score 20; DB 6; Length 3229;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1958 GGAGCTAACATCTCCAAAGTC 1939

RESULT 13
 US-10-084-817-113/C
 ; Sequence 113, Application US/10084817
 ; Publication No. US20030119009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Stuart
 ; APPLICANT: Jed G. Nuchtern
 ; APPLICANT: Sharon E. Plon
 ; APPLICANT: Jason M. Shohet
 ; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
 ; FILE REFERENCE: PA-0046 US
 ; CURRENT APPLICATION NUMBER: US/10/084,817
 ; CURRENT FILING DATE: 2002-02-25
 ; PRIORITY NUMBER: 60/270,784
 ; PRIORITY FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 365
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 113
 ; LENGTH: 3229
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030119009A1 1250434CB1
 US-10-084-817-113

Query Match 100.0%; Score 20; DB 6; Length 3229;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1958 GGAGCTAACATCTCCAAAGTC 1939

RESULT 14
 US-10-247-671-19/c
 ; Sequence 19, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mixita, Thomas
 ; APPLICANT: Shiffman, David
 ; APPLICANT: Porter, Gordon, J.
 ; APPLICANT: Keer, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
 ; FILE REFERENCE: PA-0050 US
 ; CURRENT APPLICATION NUMBER: US/10/247,671
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIORITY NUMBER: 60/323,784
 ; PRIORITY FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 19
 ; LENGTH: 3229
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CB1
 US-10-247-671-19

Query Match 100.0%; Score 20; DB 7; Length 3229;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGTC 20
 Db 1958 GGAGCTAACATCTCCAAAGTC 1939

RESULT 15
 US-10-304-126-13/C
 ; Sequence 13, Application US/10304126

; Publication No. US20040101058A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HYPOXIA-INDUCIBLE FACTOR 1 ALPHA EXPRESSION
; FILE REFERENCE: PTS-0070
; CURRENT APPLICATION NUMBER: US10/304,126
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO: 13
; LENGTH: 3551
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) . . . (2236)
US-10-304-126-13

Query Match 100.0%; Score 20; DB 8; Length 3551;
Best Local Similarity 100.0%; Prod. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGCTAACATCTCCAAGTC 20
Db 1719 GGAGCTAACATCTCCAAGTC 1700

Search completed: May 21, 2006, 21:48:56
Job time : 824 secs

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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 21:33:45 ; Search time 13.5 Seconds
(without alignments)

104.527 Million cell updates/sec

Title: US-10-766-185-4

Perfect score: 20

Sequence: 1 ggagctaacatccaaatgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB Seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New:
 1: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US09_NEW_PUB.seq*
 2: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US06_NEW_PUB.seq*
 3: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US07_NEW_PUB.seq*
 4: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US08_NEW_PUB.seq*
 5: /EMC_Celerra_SIDS3_ptodata/2/pubnra/PCT_NEW_PUB.seq*
 6: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US10_NEW_PUB.seq*
 7: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US11_NEW_PUB.seq*
 8: /EMC_Celerra_SIDS3_ptodata/2/pubnra/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	15.4	77.0	25	7	US-11-217-529-23140		Sequence 23140, A
2	15.4	77.0	1080	7	US-11-217-529-1559		Sequence 1559, Ap
3	15.2	76.0	25	7	US-11-217-529-107428		Sequence 107428,
c 4	15.2	76.0	590	6	US-10-488-619-2776		Sequence 2776, Ap
5	15.2	76.0	630	7	US-11-217-529-1916		Sequence 3916, Ap
6	15.2	76.0	1080	7	US-11-117-529-77549		Sequence 77549, A
7	14.8	74.0	2823	7	US-11-217-529-1032		Sequence 4032, Ap
8	14.8	74.0	6075	7	US-11-217-529-3047		Sequence 3047, Ap
9	14.4	72.0	2397	7	US-11-217-529-254		Sequence 254, App
10	14.2	71.0	432	7	US-11-217-529-3519		Sequence 2519, Ap
c 11	14.2	71.0	537	7	US-11-301-554-1175		Sequence 1175, Ap
12	14.2	71.0	1710	7	US-11-024-544A-58		Sequence 58, App
c 13	14.2	71.0	1710	7	US-11-190-750-35		Sequence 35, App
c 14	14.2	71.0	5105	7	US-11-024-544A-82		Sequence 82, App
c 15	14.2	71.0	5105	7	US-11-190-750-63		Sequence 63, App
c 16	14.2	71.0	5105	7	US-11-264-784-157		Sequence 157, App
c 17	14.2	71.0	6457	7	US-11-264-784-117		Sequence 117, App
c 18	14.2	71.0	7145	7	US-11-264-784-121		Sequence 121, App
c 19	14.2	71.0	7323	7	US-11-024-544A-168		Sequence 168, App
c 20	14.2	71.0	7323	7	US-11-024-545-68		Sequence 68, App
c 21	14.2	71.0	7323	7	US-11-251-466-53		Sequence 53, App
c 22	14.2	71.0	7323	7	US-11-254-173-61		Sequence 61, App
c 23	14.2	71.0	7323	7	US-11-264-784-140		Sequence 140, App
c 24	14.2	71.0	7822	7	US-11-024-544A-144		Sequence 144, App
c 25	14.2	71.0	7822	7	US-11-264-784-153		Sequence 153, App

ALIGNMENTS

RESULT 1
US-11-217-529-23140
 Sequence 23140, Application US/11217529
 ; Publication No. US0060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; ATTORNEY: NAKAO, YOSHIHIRO
 ; ATTORNEY: NAKAMURA, NORIHIRO
 ; ATTORNEY: KODAMA, YUKIKO
 ; ATTORNEY: FUJIMURA, TOMOKO
 ; ATTORNEY: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217-529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 23140
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 ; US-11-217-529-23140

RESULT 2
US-11-217-529-1559
 Sequence 1559, Application US/11217529
 ; Publication No. US0060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; ATTORNEY: NAKAO, YOSHIHIRO
 ; ATTORNEY: NAKAMURA, NORIHIRO
 ; ATTORNEY: KODAMA, YUKIKO
 ; ATTORNEY: FUJIMURA, TOMOKO
 ; ATTORNEY: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217-529

CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1559
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-1559

Query Match 77.0%; Score 15.4; DB 7; Length 1080;
Best Local Similarity 94.1%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCTAACATCCTCCAACTC 20
Db 1030 GCTGATGATCCTCCAACTC 1046

RESULT 3
US-11-217-529-107428
Sequence 107428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIORITY FILING DATE: 2005-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 107428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-107428

Query Match 77.0%; Score 15.4; DB 7; Length 1080;
Best Local Similarity 94.1%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCTAACATCCTCCAACTC 20
Db 1030 GCTGATGATCCTCCAACTC 1046

RESULT 5
US-11-217-529-3916
Sequence 3916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIORITY FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 3916
; LENGTH: 630
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-3916

Query Match 76.0%; Score 15.2; DB 7; Length 630;
Best Local Similarity 85.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCTCCAACTC 20
Db 5 GGTCCTAAGTCACCAAGTC 24

RESULT 6
US-11-217-529-77549
Sequence 77549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIORITY FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 77549
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*

US-11-217-529-77549

Query Match 76.0%; Score 15.2; DB 7; Length 1080;
Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCCTCCAACTC 20
Db 5 GGTCCTAAGTCACCAAGTC 24

US-11-217-529-254 Application US/11217529
 Sequence 254, Application US/11217529
 Publication No. US20060099612A1

GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 ADDRESS: NAKAMURA, NORIHIRO
 ADDRESS: KODAMA, YUKIKO
 ADDRESS: FUJIMURA, TOMOKO
 ADDRESS: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 4032
 LENGTH: 2823
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-4032

Query Match 1 GGAGCTAACATCTCCAG 18
 Best Local Similarity 88.9%; Pred. No. 28;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 192 GGAACTAACATCTCCAG 209

RESULT 7
 US-11-217-529-4032
 Sequence 4032, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 ADDRESS: NAKAMURA, NORIHIRO
 ADDRESS: KODAMA, YUKIKO
 ADDRESS: FUJIMURA, TOMOKO
 ADDRESS: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 4032
 LENGTH: 2823
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-4032

Query Match 1 GGAGCTAACATCTCCAG 18
 Best Local Similarity 88.9%; Pred. No. 28;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 192 GGAACTAACATCTCCAG 209

RESULT 8
 US-11-217-529-3047
 Sequence 3047, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 ADDRESS: NAKAO, YOSHIHIRO
 ADDRESS: NAKAMURA, NORIHIRO
 ADDRESS: KODAMA, YUKIKO
 ADDRESS: FUJIMURA, TOMOKO
 ADDRESS: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 3047
 LENGTH: 6075
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-3047

Query Match 1 GGAGCTAACATCTCCAG 19
 Best Local Similarity 88.3%; Pred. No. 32;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 3391 GAGGCTAACATCTCCAGT 3408

RESULT 9
 US-11-217-529-2519
 Sequence 2519, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 ADDRESS: NAKAO, YOSHIHIRO
 ADDRESS: NAKAMURA, NORIHIRO
 ADDRESS: KODAMA, YUKIKO
 ADDRESS: FUJIMURA, TOMOKO
 ADDRESS: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE: 2005-09-02
 PRIORITY FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 2519
 LENGTH: 432
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*
 US-11-217-529-2519

Query Match 1 GGAGCTAACATCTCCAGT 19
 Best Local Similarity 84.2%; Pred. No. 41;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 202 GAAGCTAACATCATCAGT 220

RESULT 11
 US-11-301-54-1175/C
 Sequence 1175, Application US/11301554
 Publication No. US20060088527A1
 GENERAL INFORMATION:
 APPLICANT: Henderson, Robert A.

1 APPLICANT: wang, Tongtong
 1 APPLICANT: Watanabe, Yoshihiro
 1 APPLICANT: Kallen, Michael D.
 1 APPLICANT: Sleath, Paul R.
 1 APPLICANT: Johnson, Jeffrey C.
 1 APPLICANT: Retter, Marc W.
 1 APPLICANT: Durham, Margarita
 1 APPLICANT: Carter, Derrick
 1 APPLICANT: Fanger, Gary R.
 1 APPLICANT: Vedlick, Thomas S.
 1 APPLICANT: Bangur, Chaitanya S.
 1 APPLICANT: McNabb, Andria
 1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 1 FILE REFERENCE: 210121.478621
 1 CURRENT APPLICATION NUMBER: US/11/301,554
 1 CURRENT FILING DATE: 2005-12-13
 1 PRIOR APPLICATION NUMBER: US/10/283,017
 1 PRIOR FILING DATE: 2002-10-28
 1 PRIOR APPLICATION NUMBER: US/10/113,872
 1 PRIOR FILING DATE: 2002-03-28
 1 PRIOR APPLICATION NUMBER: US/10/017,754
 1 PRIOR FILING DATE: 2001-10-29
 1 PRIOR APPLICATION NUMBER: US/09/902,941
 1 PRIOR FILING DATE: 2001-07-10
 1 PRIOR APPLICATION NUMBER: US/09/849,526
 1 PRIOR FILING DATE: 2001-05-03
 1 PRIOR APPLICATION NUMBER: US/09/736,457
 1 PRIOR FILING DATE: 2000-12-13
 1 PRIOR APPLICATION NUMBER: US/09/702,705
 1 PRIOR FILING DATE: 2000-10-30
 1 PRIOR APPLICATION NUMBER: US/09/677,419
 1 PRIOR FILING DATE: 2000-10-06
 1 PRIOR APPLICATION NUMBER: US/09/671,325
 1 PRIOR FILING DATE: 2000-09-26
 1 NUMBER OF SEQ ID NOS: 2157
 1 SEQUENCE ID NO: 1175
 1 LENGTH: 537
 1 TYPE: DNA
 1 ORGANISM: Homo sapiens
 1 US-11-301-554-1175

1 Query Match 71.0%; Score 14.2%; DB 7; Length 537;
 1 Best Local Similarity 81.2%; Pred. No. 43; *
 1 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGCTAACATCTCCAAAGT 19
 Db 499 GGAGCTGACTTCGCCAAAGT 481

RESULT 12
 US-11-024-544A-58
 1 Sequence 58, Application US/11/024544A
 1 Publication No. US20060094086A1
 1 GENERAL INFORMATION:
 1 APPLICANT: E.I. dupont de Nemours and Company, Inc.
 1 APPLICANT: Yadav, Narendra
 1 APPLICANT: Xue, Zhixiang
 1 APPLICANT: Zhang, Hongxiang
 1 TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
 1 FILE REFERENCE: CL217
 1 CURRENT APPLICATION NUMBER: US/11/024,544A
 1 CURRENT FILING DATE: 2004-12-29
 1 NUMBER OF SEQ ID NOS: 175
 1 SOFTWARE: PatentIn version 3.3
 1 SEQ ID NO: 58
 1 LENGTH: 1710

1 Query Match 71.0%; Score 14.2%; DB 7; Length 1710;
 1 Best Local Similarity 84.2%; Pred. No. 52;
 1 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAAGTC 20
 Db 404 GAGCTAACGTCCACAGTC 422

RESULT 13
 US-11-190-750-35
 1 Sequence 35, Application US/11/190750
 1 Publication No. US20060034088A1
 1 GENERAL INFORMATION:
 1 APPLICANT: E.I. dupont de Nemours and Company, Inc.
 1 APPLICANT: Picataggio, Stephen K.
 1 APPLICANT: Yadav, Narendra
 1 APPLICANT: Zhang, Hongxiang
 1 TITLE OF INVENTION: ACTYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
 1 POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
 1 OLEAGINOUS ORGANISMS
 1 FILE REFERENCE: CL218
 1 CURRENT APPLICATION NUMBER: US/11/190,750
 1 CURRENT FILING DATE: 2005-07-27
 1 NUMBER OF SEQ ID NOS: 159
 1 SOFTWARE: PatentIn version 3.3
 1 SEQ ID NO: 35
 1 LENGTH: 1710
 1 TYPE: DNA
 1 ORGANISM: Yarrowia lipolytica
 1 US-11-190-750-35

Query Match 71.0%; Score 14.2%; DB 7; Length 1710;
 Best Local Similarity 84.2%; Pred. No. 52;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCTAACATCTCCAAAGTC 20
 Db 404 GAGCTAACGTCCACAGTC 422

RESULT 14
 US-11-024-544A-82/C
 1 Sequence 82, Application US/11/024544A
 1 Publication No. US20060094086A1
 1 GENERAL INFORMATION:
 1 APPLICANT: E.I. dupont de Nemours and Company, Inc.
 1 APPLICANT: Yadav, Narendra
 1 APPLICANT: Xue, Zhixiang
 1 APPLICANT: Zhang, Hongxiang
 1 TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATE
 1 FILE REFERENCE: CL217
 1 CURRENT APPLICATION NUMBER: US/11/024,544A
 1 CURRENT FILING DATE: 2004-12-29
 1 NUMBER OF SEQ ID NOS: 175
 1 SOFTWARE: PatentIn version 3.3
 1 SEQ ID NO: 82
 1 LENGTH: 5105
 1 TYPE: DNA
 1 ORGANISM: Artificial Sequence
 1 FEATURE:
 1 OTHER INFORMATION: Plasmid pLV13
 1 FEATURE:
 1 NAME/KEY: misc feature
 1 LOCATION: (4446)..(4446)
 1 OTHER INFORMATION: n is a, c, g, or t
 1 US-11-024-544A-82

Query Match 71.0%; Score 14.2; DB 7; Length 5105;
 Best Local Similarity 84.2%; Pred. No. 63; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;

Qy 2 GAGCTAACATCTCCAGTC 20
 Db 3692 GAGCTAACCTCCAGTC 3674

RESULT 15

US-11-190-750-63/C

Sequence 63, Application US/11190750

Publication No. US2006009408A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Company, Inc.

APPLICANT: Picataggio, Stephen K.

APPLICANT: Yadav, Narendra

APPLICANT: Zhang, Hongxiang

TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF OLEAGINOUS ORGANISMS

FILE REFERENCE: CL2718

CURRENT APPLICATION NUMBER: US/11/190,750

CURRENT FILING DATE: 2005-07-27

NUMBER OF SEQ ID NOS: 159

SOFTWARE: Patentin version 3.3

SEQ ID NO 63

LENGTH: 5105

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Plasmid pLV13

FEATURE:

NAME/KEY: misc_feature

LOCATION: (4446)..(4446)

OTHER INFORMATION: n is a, c, g, or t

US-11-190-750-63

Query Match 71.0%; Score 14.2; DB 7; Length 5105;
 Best Local Similarity 84.2%; Pred. No. 63; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;

Qy 2 GAGCTAACATCTCCAGTC 20
 Db 3692 GAGCTAACCTCCAGTC 3674

Search completed: May 21, 2006, 21:34:20
 Job time : 14.5 secs

Type of Search	*****	Searcher:	*****
NA#:	AA#:	Date Searcher Picked up:	Online Time:
S/L:	Oligomer:	Searcher Phone:	Searcher Prep Time:
Encode/Transl:	Text:	Inventor:	WWW/Internet:
QUESTEL/ORBIT:	Ligation:	Other (Specify):	Other (Specify):
DIALOG:			
STN:			
Vendors and cost where applicable	*****		
*****	*****		

Thank You

Ple

984'99/01

Please, a length limited search of SEQ ID NOS: 2 and (4 nt ≤ 50). Please also a standard search of SEQ ID NOS: 2 and 4.

Sean McGarry 73484
AU 1635
571.272.0761
REM C18 Mailbox
PHP

From: Sean McGarry [mailto:sean.mcgarry@stfc.ac.uk]
Sent: Tuesday, May 16, 2006 12:44 PM
To: chelmib@stfc.ac.uk
Subject: RE: SEARC10/766185

STIC-BioTech/CheMlib